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(54) **DNA microarray for rapid identification of Candida albicans in blood cultures.**

(57) The present invention provides a DNA microarray for identification and characterisation of microorganisms in a sample or clinical specimen. Furthermore, it provides for a method for rapid identification and strain

profiling of different microbial species in clinical specimens, especially in blood cultures, utilizing said DNA microarray.

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Description

[0001] The present invention provides a DNA microarray for identification and characterisation of microorganisms in a sample or clinical specimen. Furthermore, it provides for a method for rapid identification and strain profiling of different microbial species in clinical specimens, especially in blood cultures, utilizing said DNA microarray.

Background

[0002] Isolation, identification and characterisation of bacteria from clinical specimens is a main task of microbiological routine diagnostics. In fact, microorganisms are ubiquitous in certain areas of the human body. For this reason isolation and identification of pathogenic bacteria from clinical material and discrimination of specific pathogens from contaminations with indigenous or environmentally encountered microorganisms is a requirement for the correct diagnosis of infectious diseases. Additionally, accurate identification of antibiotic resistance and particular virulence factors provide important information enabling the clinician to choose effective antimicrobial therapy.

[0003] In the course of infection, many specimen types can be used for direct identification of the pathogens. These include, but are not limited to, liquor in the course of bacterial meningitis, sputum from patients with bacterial pneumonia, urine in the course of upper and lower urinary tract infections, punctate from sites of deep purulent infections (such as abscess, phlegmone, lung emphysema and septic arthritis), stool from patients with gastrointestinal tract infections, pus or wound fluid from purulent infections of the skin and wounds. Sometimes, bacteria are represented in the specimen only in minor numbers, thus, indirect identification of pathogens after culture of specimens in liquid media is employed. Important examples are enrichment cultures of food samples during outbreaks of food borne infections and blood cultures for diagnosis of bloodstream infections.

[0004] The invasion of the bloodstream by microorganisms, especially bacteremia and fungemia, represents one of the most serious consequences of infections and is a high ranked cause of death (Mylotte, J.M. and Tayara, A., Eur. Clin. Microbiol. Infect. Dis. 19:157-163 (2000); Reimer, L.G. et al., Clin. Microbiol. Rev. 10:444-465 (1997)). Bacteremia is the means by which local infections spread hematogenously to distant organs. This hematogenous dissemination of bacteria is part of the pathophysiology of, e.g., meningitis and endocarditis, Pott's disease and many other forms of osteomyelitis. In the hospital, indwelling catheters are a frequent cause of bacteremia and subsequent nosocomial infections, since they provide a means by which bacteria normally found on the skin can enter the bloodstream. Other causes of bacteremia include dental procedures, urinary tract infections, intravenous drug use, and colorectal cancer.

[0005] Systemic fungal infection is becoming more and more common in modern hospitals. The most common fungal infections are candidiasis and aspergillosis, but other systemic fungal infections such as Histoplasmosis, Blastomycosis, Coccidioidomycosis and Cryptococcosis are also of increasing relevance. Systemic fungal infections in hospitals are commonly seen in immune compromised patients and - like bacteremia - in patients with indwelling catheters. Due to underlying serious illnesses and possible resistance of the pathogens to antifungal agents, patients with systemic fungal infections often have poor clinical outcomes. Infections due to *Candida* species are the fourth most important cause of nosocomial bloodstream infection.

[0006] Bacteremia is operationally defined as the presence of viable bacteria as evidenced by positive blood cultures. Fungemia is similarly defined as the presence of viable fungi as evidenced by positive blood cultures. When bacteremia or fungemia occurs in the presence of systemic symptoms (such as fever or chills) the condition is designated as sepsis; and in the setting of more severe disturbances of temperature, respiration, heart rate or white blood cell count, is characterised as systemic inflammatory response syndrome (SIRS).

[0007] Many septic episodes are nosocomial and often due to microorganisms with increased and multiple antimicrobial resistance. *Staphylococcus aureus*, *Escherichia coli*, Coagulase-negative staphylococci (CoNS), *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus* spp., *Streptococcus* spp., *Candida albicans* and *Enterobacter cloacae* are the most frequent etiological agents of bacteremia and fungemia in Europe (Decousser, J. W. et al., J. Antimicrob. Chemother. 51:1214-22 (2003); Lyytikäinen, O. et al., Clin. Infect. Dis. 35:314-9 (2002); Reacher, M.H. et al., BMJ 320: 213-6 (2000); Rosenthal Kreuberger, E.J., Int. J. Antimicrob. Agents 24:196-8 (2004)) and the USA (Bourbeau, P.P. and Pohlman, J.K., J. Clin. Microbiol. 39:2079-82 (2001); Reimer, L.G. et al., Clin. Microbiol. Rev. 10:444-65 (1997); Reisner, L.G. et al., J. Clin. Microbiol. 37:2024-6 (1999); Wilson, M.L. et al., J. Clin. Microbiol. 37:1709-13 (1999)).

[0008] Nosocomial bacteremia and especially sepsis require an immediate antibiotic therapy, even when the causative bacteria are still unknown. Thus, said therapy has to be performed as empirical initial therapy (Rello, J. et al., Intensive Care Med. 20:94-98 (1994)), which covers the complete spectrum of relevant pathogens. However, the increase of bacterial resistance lowers the chance of success for such empirical antibiotic treatments considerably (Mylotte, J.M. and Tayara, A., Eur. Clin. Microbiol. Infect. Dis. 19:157-163 (2000); Weinstein, M.P. et al., Clin. Infect. Dis. 24:584-602 (1997)). This primary therapy can only be replaced by a specific treatment after a thorough microbial diagnosis which usually takes 76-120 h (Bourbeau, P.P. and Pohlman, J.K., J. Clin. Microbiol. 39:2079-2082 (2001)). A fast track diagnosis which shortens this lag time would increase the chance of therapy success.

[0009] Rapid and reliable detection of bloodstream infections, including characterisation of the pathogen to the species level and determination of its antibiotic susceptibility pattern, is crucial for several reasons: (i) Appropriate antimicrobial agents can be selected, and thus, unnecessary treatment with ineffective antibiotics can be avoided; (ii) the prognosis of the patients can be improved; (iii) the acquisition of resistances in pathogens may be decelerated and (iv) expenditures on antimicrobials and overall hospital costs can be reduced (Barenfanger, J. et al., J. Clin. Microbiol. 37:1415-8 (1999) ; Doern, G.V. et al., J. Clin. Microbiol. 32:1757-62 (1994); Trenholme, G.M. et al., J. Clin. Microbiol. 27:1342-5 (1989); Wheeler, A.P. and Bernard, G.R., N. Engl. J. Med. 340:207-14 (1999)). Therefore, there is a strong need for rapid tests for specific and sensitive identification of bacteria and pathogenic fungi directly from blood cultures.

[0010] The diagnosis of bacteremia commonly relies on blood cultures where the growth of microorganisms is continuously monitored by automated devices (James, P.A. and Al-Shafi, K.M., J. Clin. Pathol. 53:231-233 (2000); Reisner, B.S. and Woods, G.L., J. Clin. Microbiol. 37:2024-2026 (1999); Wilson, M.L. et al., J. Clin. Microbiol. 37:1709-1713 (1999)). Although such continuous-reading and computed systems decrease the time for detection of positive blood cultures, definitive pathogen identification from positive blood cultures still requires traditional Gram-staining, sub-culturing and susceptibility testing, delaying the identification of pathogens for one to three days (Levi, K and Townner, K.J., J. Clin. Microbiol. 41:3890-3892 (2003); Oliveira, K. et al., J. Clin. Microbiol. 41:889-891 (2003); Oliveira, K. et al., J. Clin. Microbiol. 40:247-251 (2002); Tan, T.Y. et al., J. Clin. Microbiol. 39:4529-4531 (2001)). The subculture procedure with subsequent species identification and determination of antibiotic resistance is time-consuming and elaborate. The biochemical and immunological assays like testing with coagulase, nuclease or latex agglutination are not always reliable. Antigenic and biochemical variations of bacteria grown in blood culture, inhibitory action of blood culture medium components as well as the presence of more than one microbial species may mislead data interpretation.

[0011] Staphylococci are the most important and frequent group of pathogens growing in blood culture, responsible for 30% to more than 50% of all bacteremia events (James, P.A. and Al-Shafi, K.M., J. Clin. Pathol. 53:231-233 (2000) ; Reisner, B.S. and Woods, G.L., J. Clin. Microbiol. 37:2024-2026 (1999); Velasco, E. et al., Sao Paulo Med. J. 118: 131-138 (2000)) with a mortality rate ranging from 13 to 50% (McClelland, R.S. et al., Arch. Intern. Med. 159:1244-1247 (1999); Rello, J. et al., Intensive Care Med. 20:94-98 (1994); Weinstein, M.P. et al., Clin. Infect. Dis. 24:584-602 (1997)). The emergence of *S. aureus* strains with multiple resistance to antibiotics makes empirical therapy prone to fail (Tan, T.Y. et al., J. Clin. Microbiol. 39:4529-4531 (2001)). *S. aureus* is generally regarded as a virulent pathogen, whereas CoNS are either considered as a cause of catheter-associated nosocomial bacteremia or, more frequently, as blood culture contamination. Thus, a subgenus identification of gram-positive cocci in clusters (CPCC) is of great clinical significance (Oliveira, K. et al., J. Clin. Microbiol. 41 :889-891 (2003)).

[0012] Methods used up to date for direct identification of *S. aureus* growing in blood culture bottles include biochemical tests, like detection of thermostable nuclease or tube coagulase test, or commercial antibody-based kits connected with the disadvantages listed above.

[0013] Besides *S. aureus* and coagulase-negative staphylococci, *E. coli*, *Klebsiella* spp., *Enterobacter* spp., *Proteus* spp. and *P. aeruginosa* belong to the most frequent reported pathogens causing bacteremia (Reimer, L.G. et al., Clin. Microbiol. Rev., 10:444-65 (1997); Reacher, M.H. et al., BMJ, 320:213-6 (2000); Lyytikäinen, O. et al., Clin. Infect. Dis., 35:e14-9 (2002)). In order to reduce the time needed for identification and susceptibility testing, the possibility of combining an automated blood culture system with an automated identification and susceptibility testing system by direct inoculation from positive blood cultures has been studied for gram-positive cocci as well as for gram-negative rods by several groups of investigators, but with varying success (Reimer, L.G. et al., Clin. Microbiol. Rev., 10:444-65 (1997); Hansen, D.S. et al., Clin. Microbiol. Infect., 8:38-44 (2002); Ling, T.K. et al., J. Clin. Microbiol., 41:4705-7 (2003); Funke, G. and Funke-Kissling, P., J. Clin. Microbiol., 42:1466-70 (2004)). Although the authors saw some potential of the combined system to allow the agar isolation step to be skipped, the system is hampered by the fact that (i) the blood culture sample has to undergo a time-consuming separation procedure for the enrichment of bacterial cells, (ii) the identification rate varies depending on the employed identification system and (iii) the performance is not equally good for gram-negative and gram-positive pathogens (Reimer, L.G. et al., Clin. Microbiol. Rev., 10:444-65 (1997); Ling, T.K. et al., J. Clin. Microbiol., 41:4705-7 (2003); Funke, G. and Funke-Kissling, P., J. Clin. Microbiol., 42:1466-70 (2004)).

[0014] Considerable progress was made using nucleic acid-based methods for the identification and genotyping of bacteria or fungi in blood specimens. Assays employing ribosomal RNA-based oligonucleotide probes like fluorescence *in situ* hybridisation (FISH) (Chapin, K. and Musgnug, M., J. Clin. Microbiol. 41:4324-7 (2003); Jansen, G.J. et al., J. Clin. Microbiol. 38:814-7 (2000); Kempf, V.A. et al., J. Clin. Microbiol. 38:830-8 (2000); Oliveira, K. et al., J. Clin. Microbiol. 41:889-91 (2003)) or microarrays (Anthony, R.M. et al., J. Clin. Microbiol. 38:781-8 (2000); Marlowe, E.M. et al., J. Clin. Microbiol. 41 :5127-33 (2003); Sogaard, M. et al., J. Clin. Microbiol., 43:1947-9 (2005)) provide for rapid species identification in blood cultures. However, methods solely based on ribosomal RNA probes allow species identification only, and do not provide information on antibiotic susceptibility and other strain specific characteristics (e.g. virulence genes). For the molecular detection of antibiotic resistances in staphylococci, several multiplex PCR-based assays were described (Martineau, F. et al., Antimicrob. Agents Chemother. 44:231-8 (2000); Shrestha, N.K. et al., Approved standard M2-4A, Villanova, PA (1990); Strommenger, B.C. et al. J. Clin. Microbiol. 41:4089-94; Tan, T.Y. et al., J. Clin. Microbiol.

39:4529-31 (2001)). Several groups have successfully identified *S. aureus* and more specifically methicillin-resistant *S. aureus* strains (MRSA) from blood cultures by using DNA probes (Levi, K. and Towner, K.J., J. Clin. Microbiol. 41: 3890-3892 (2003); Poulsen, A.B. et al., J. Antimicrob. Chemother. 51 :419-421 (2003)), peptide nucleic acid probes (Oliveira, K. et al., J. Clin. Microbiol. 41 :889-891 (2003)), multiplex PCR (Mason, W. J. et al., J. Clin. Microbiol. 39: 3332-3338 (2001)), gel-based PCR (Krishnan, P.U. et al., J. Clin Pathol. 55:745-748 (2002)), and real-time PCR (Shrestha N.K. et al., J. Clin. Microbiol. 40:2659-2661 (2002); Tan, T.Y. et al., J. Clin. Microbiol. 39:4529-4531 (2001)).

[0015] However, the use of such molecular assays suffers from two main restrictions: First, they rely on a pre-identification of the pathogen since their discriminatory capacity is technically limited, for instance by the number of fluorochromes available for labelling the probes or, in the case of multiplex PCR, by the capacity of resolution in gel electrophoresis. These molecular assays are thus usually not scalable and unfit for high throughput analysis.

[0016] The last years have witnessed the emergence of many DNA microchip projects arraying genes of microorganisms (Ye, R.W. et al., J. Microbiol. Methods 47:257-272 (2001)). They can detect tens of thousands of DNA sequences in a single hybridisation step (DeRisi, J.L. et al., Science 278:680-686 (1997); Duggan, D.J. et al., Nat. Genet. 21:10-14 (1999); Lashkari, D.A. et al., Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997)). Originally developed for gene expression profiling, DNA sequence analysis and genotyping, microarrays were recently also used to identify viral (Wang, R.F. et al., FEMS Microbiol. Lett. 213:175-182 (2002)) and bacterial (Bekal, S. et al., J. Clin. Microbiol. 41 :2113-2125 (2003)) pathogens in environmental and clinical samples.

[0017] Most of the published reports employed oligonucleotide microarrays containing a reduced number of spotted probes and representing a single bacterial species only (Volokhov, D. et al., J. Appl. Microbiol. 95:787-798 (2003); Volokhov, D. et al., J. Clin. Microbiol. 41:4071-4080 (2003); Volokhov, D. et al., J. Clin. Microbiol. 40:4720-4728 (2002)). Such arrays were used to identify pathogenic strains belonging to a pre-identified species (Chizhikov, V. et al., Appl. Environ. Microbiol. 67:3258-3263 (2001)), to distinguish between species of the same genus (Volokhov, D. et al., J. Clin. Microbiol. 41:4071-4080 (2003); Volokhov, D. et al., J. Clin. Microbiol. 40:4720-4728 (2002)) or to detect genes encoding resistance to a certain antibiotic (Volokhov, D. et al., J. Appl. Microbiol. 95:787-798 (2003)).

[0018] Although such specific short-oligonucleotide microarrays could be rapidly designed and built up they carry some intrinsic disadvantages: like all methods based on single and often short DNA sequences they show reduced reliability and sensitivity (Stears, R.L. et al., Nat. Med. 9:140-145 (2003)). To palliate the high probability of non-specific hybridisation due to their short size (20-40bp) it is necessary to design many partially overlapping oligonucleotides in order to confirm the presence of a gene. This consequent increase in complexity makes it extremely difficult to set up the optimal hybridisation conditions necessary for producing trustful results. Moreover, surface-bound short oligonucleotides have poor hybridisation properties and are highly sensitive to single nucleotide polymorphisms (Hughes, T.R. et al., Nat. Biotechnol. 19:342-347 (2001)). For these reasons, oligonucleotide micro-arrays are unsuitable for routine diagnostics.

[0019] Up to now, diagnosis of bacteremia by microarrays is limited to species identification by oligonucleotides for 23S RNA sequences, which is still strictly experimental (Anthony, R.M. et al., J. Clin. Microbiol. 38:781-788 (2000)) and carries along the methodological weakness associated to the use of oligonucleotides as hybridisation probes.

[0020] A DNA microarray employing capture probes of more than 40 nt length amplified by PCR was described by Fitzgerald et al. (Fitzgerald, J.R. et al., Proc. Natl. Acad. Sci. USA 98(15):8821-8826 (2001)). To investigate molecular population genetics of *Staphylococcus aureus* on a genome scale, a microarray comprising 2817 complete ORFs of *S. aureus* strain COL was constructed, representing >90% of the *S. aureus* genome. The microarray was able to discriminate 36 *S. aureus* strains. However, since it was not designed for the identification of different bacterial species, it was not tested for possible cross reactions with other bacteria besides *S. aureus*. Due to the conservative nature of many house-keeping proteins and genes, respectively, cross reactions of the microarray with CoNS strains and other bacterial species will occur. Unspecific cross reactions combined with the high number of probes (2817) result in a high complexity of the microarray data, not applicable to routine diagnostics. Furthermore, PCR amplification of long ORFs is a difficult procedure, in particular for bacteria with DNA of high GC-content.

[0021] The aim of present invention is to provide a gene-segment based microarray for identification and characterisation of different microorganisms, especially different bacteria and pathogenic fungi, present in a sample or clinical specimen.

Summary of the Invention

[0022] The present invention provides a DNA microarray for the identification and characterisation of microorganisms in biological samples, especially of microorganisms connected with bacteremia, fungemia and sepsis. Species specific gene probes in this microarray allow the identification of different microbial species, whilst antibiotic resistance and virulence gene probes allow for the genotypic discrimination within a species. The microarray can be designed to allow species identification, virulence determination and resistance determination independently from each other or simultaneously, and furthermore said determinations can be performed for one or more different microbial species and strains

with one microarray. Furthermore, different microbial species and strains are discriminated, even in a polymicrobial sample (specimen with more than one pathogen).

[0023] The DNA microarray according to present invention thus demonstrates the feasibility of simultaneously identifying and characterising different microbial species in a sample or clinical specimen, especially in blood samples, without prior PCR amplification of target DNA or pre-identification of the pathogen. This can reduce sample processing time to a single day and less.

[0024] The invention furthermore provides a method for rapid identification and characterisation of microorganisms, especially of bacteria, yeasts and filamentous fungi, using the microarray of the invention. The method is quick, can be automated, leads to reproducible results and allows an early choice of specific antibiotics for treatment of bacteremia, fungemia or sepsis.

[0025] In particular, the present invention provides

(1) a DNA microarray for direct identification and characterisation of microorganisms in a sample or clinical specimen, wherein the microarray comprises gene probes being derived from DNA sequences or partial DNA sequences of the microorganisms to be identified or DNA sequences complementary or homologous thereto and having a length of at least 100 nucleotides (nt);

(2) the use of the DNA microarray as defined in (1) above for *in vitro* identification and characterisation of microorganisms in a sample or in a clinical specimen, preferably for the diagnosis of bacteremia, fungemia or sepsis;

(3) an *in vitro* method for identification and characterisation of microorganisms in a sample or in a clinical specimen comprising

(a) isolating the total DNA from the sample or clinical specimen and labelling the DNA with a reporter molecule, preferably a fluorochrome;

(b) applying the DNA thus obtained to the DNA microarray as defined in (1) above and hybridising the DNA with the gene probes of the DNA microarray; and

(c) detecting DNA bound to the DNA microarray by determination of the amount of the reporter molecules bound to the array; and

(4) a kit for detection of microorganisms in a sample or clinical specimen comprising the microarray of embodiment (1).

Brief description of the Figures

[0026]

Fig. 1: DNA microarray analyses of 58 clinical isolates, reference strains and blood cultures.

Each column shows the results of an individual hybridisation with target DNA prepared from: *S. aureus* ATCC 29213 (1), MW2 (2), clinical isolates (3-7), positive blood cultures (8-11); *P. aeruginosa* ATCC 27853 (12), clinical isolates (13-17), positive blood culture (18); *E. coli* ATCC 25922 (19), clinical isolates (20-25), positive blood cultures (26-27); *S. epidermidis* clinical isolates (28-32), positive blood cultures (33-35); clinical isolates of *S. auricularis* (36), *S. capitis* (37), *S. haemolyticus* (38), *S. hominis* (39), and *S. warneri* (40). Other Gram-negative species included a *Proteus mirabilis* positive blood culture (41), clinical isolates of *Proteus mirabilis* (42-43), *Serratia marcescens* (44-45), *Klebsiella pneumoniae* (46-48), *Stenotrophomonas maltophilia* (49), *Acinetobacter baumannii* (50), *Enterobacter cloacae* (51) and *Enterobacter aerogenes* (52); other Gram-positive species included clinical isolates of *Micrococcus* spp. (53), *Enterococcus* spp. (54), *Enterococcus faecalis* (55) and *Streptococcus pneumoniae* (56) and two positive blood cultures of *S. pneumoniae* (57-58).

(A) Hybridisation of DNA prepared from bacterial isolates, reference strains and blood cultures with *E. coli* gene probes;

(B) hybridisation with *P. aeruginosa* gene probes;

(C) hybridisation with *S. aureus* gene probes.

Grey boxes represent gene probes which hybridised with the respective target DNA, white boxes represent gene probes which showed no hybridisation with the respective target DNA.

Fig. 2: Validation of the *S. aureus* microarray of example 11. 2 µg genomic DNA from *S. aureus* strain T94 were labelled either with Cy3 or Cy5, combined and hybridised as described in Example 11. Cy3: green signal; Cy5: red signal; double-hybridisation: yellow signal.

- A) Overlay of microarray scanned using Cy3 and Cy5 filter sets;
 B) Scatterplot of normalized fluorescence intensities of individual gene probes after microarray hybridisation.
 The signal intensities from both channels correlate highly with each other ($r^2 = 0.97$).

Fig. 3: Specific identification of *S. aureus* from distantly related bacteria using the microarray of example 11. 2 µg of *S. aureus* DNA were co-hybridised with 2 µg of pure *E. coli* (A) or *P. aeruginosa* (B) genomic DNA. Obtained hybridisation patterns are represented as bar codes, where the 140 spotted gene segments appear subsequently and are clustered in categories (NC: negative control; PC: positive control; Antibiotic Resistance Determinants; Virulence Factors and Metabolic Functions (see Tab. 6)). Positive hybridisation is indicated by a bar while negative spots are represented by an empty area. Both assays show clear *S. aureus* discrimination with practically no cross hybridisation between DNA from said gram negative bacteria and *S. aureus* selected genes, while the positive control (16S RNA sequence) reveals the good quality of hybridisation.

Fig. 4: Specific identification of *S. aureus* from coagulase negative staphylococci using the microarray of example 11. 2 µg of *S. aureus* DNA were co-hybridised with 2 µg of *S. epidermidis* (A) or *S. saprophyticus* (B) genomic DNA. Obtained hybridisation patterns are illustrated by scanned fluorescent picture data (A: *S. aureus*: green signal; *S. epidermidis*: red signal; B: *S. aureus*: red signal; *S. saprophyticus*: green signal) and transformed in bar codes (see legend of Fig. 3). All specific *S. aureus* virulence factor genes hybridised exclusively with *S. aureus* DNA. Yellow spots showing cross-hybridisation correspond to some shared antibiotic resistance determinants and genes associated to metabolic functions.

Fig. 5: Specificity of the *S. aureus* microarray of example 11.

- A) Scan of microarray hybridised with 2 µg each of genomic DNA from *S. aureus* strain T103 (Cy3, represented in green) or T100 (Cy5, represented in red), showing remarkable genotypic differences between strains.
 B) PCR amplification of the genes from genomic DNA of *S. aureus* (strains T100 and T103) validating results of the microarray hybridisation shown in (A).

Fig. 6: Identification and characterisation of *S. aureus* from positive blood culture using the microarray of example 11. 2 µg of DNA prepared from blood culture positive for *S. aureus* (strain T95) was co-hybridised with 2 µg of DNA prepared from sterile blood culture or with 2 µg of pure *S. aureus* genomic DNA for 4 hours. Positive and negative spots are transformed in a bar code scheme (see legend of Fig. 3). Sterile blood culture DNA did not cross-hybridise with spotted *S. aureus* genes (A). Blood culture positive for *S. aureus* produced a fluorescent hybridisation pattern almost identical to the pattern obtained with pure *S. aureus* genomic DNA (B).

Definitions

[0027] In the framework of the present invention the following terms and definitions are used.

[0028] A "DNA microarray" consists of a collection of nucleic acid sequences, preferably DNA sequences, immobilized onto a solid support, such as glass, plastic or silicon chips, in a latticed pattern (forming an "array"). Each unique sequence of said sequences forms a tiny feature on the microarray called a "spot" or "capture probe". The size of these spots varies from one system to another, but is usually less than two hundred micrometers in diameter, thus up to tens of thousands of spots can be arrayed in a total area of a few square centimeters. DNA microarrays provide a means to detect and quantify large numbers of discrete nucleic sequences in parallel. In a microarray hybridisation the nucleic acids in the sample that is being analysed (called "target") are expected to form duplexes specifically with the corresponding capture probes. Occurrence or absence of duplex formation indicate the presence or absence of said target. For routine microarray analysis, said target is commonly converted to a labelled population of nucleic acids, using reporter molecules. Hybridisation of said labelled target DNA molecules from the tested samples with complementary DNA sequences affixed in specific spots on the array can thus be detected by examination for the presence of said label on the array using a microarray scanner (Müller, H.-J., Röder, T., "Der Experimentator: Microarrays, Spektrum Akademischer Verlag, Heidelberg (2004)).

[0029] "Gene probe" or "gene probe derived from..." refers to a DNA sequence present on the microarray of present invention and used as a capture probe. It is complementary to a target DNA sequence, preferably to a microbial, more preferably to a bacterial or fungal gene or gene segment. Said gene probe is prepared by any known method of DNA synthesis, and preferably prepared by cloning the respective PCR-amplified gene or gene segment into a plasmid/vector. The recombinant gene or gene segment is then amplified by PCR, isolated from the amplification mix, purified (preferably by ethanol-purification) and finally spotted onto the array.

[0030] A "clinical isolate" is a microbial, especially a fungal or bacterial strain isolated from a clinical specimen, wherein the isolation includes at least one *in vitro* propagation.

[0031] An "isolated DNA" is a DNA separated or purified from the organism it is naturally associated with or from the clinical specimen in which it occurs. This comprises biochemically or biophysically purified native DNA, recombinant DNA, chemically synthesized DNA and DNA analogues (e.g. peptide nucleic acids).

[0032] "Native" is synonymous to "naturally (occurring)".

[0033] A "DNA segment" or "gene segment" is an isolated DNA which contains or consists of a part of the native full-length sequence of a gene which is still able to hybridize to the native sequence under stringent hybridisation conditions. Although the present invention is in the following exclusively described as relating to "DNA" sequences, it is not to be construed as being limited thereto. Rather, if the term "DNA" is used in connection with the gene probes or target sequences of present invention, it includes other polynucleotides (like RNA or RNA/DNA hybrids), and DNA analogues such as PNA, phosphonate backbone DNA, artificial pentose or hexose backbone DNA which is able to hybridize with native DNA etc.. Furthermore, modified bases like deoxy bases, inosine or aminoallylcytosine may be used on all DNA, RNA and PNA backbones. However, DNA itself is the preferred polynucleotide for performance of the invention.

[0034] The DNA sequences used as gene probes in present invention are either identical, substantially identical or homologous to the complementary native target sequences. In the context of present invention, when a specific DNA sequence is denominated, this encompasses not only said specific sequence, but also the sequences substantially identical or homologous thereto, i.e. its substitution mutants. "Substantially identical" means that the DNA contains mutations of up to 10% of the total number of nt in comparison with the native DNA sequence and/or has a nucleotide identity of > 90% to the corresponding native DNA segment. Said mutations are preferably single nucleotide polymorphisms or point mutations and include the mutation of not only a single but also a few (up to 10 nt, preferably up to 5 nt) consecutive nt. "Homologous" or "homologue" refers to a DNA sequence which has a sequence identity of more than 70% of the corresponding native DNA sequence and encompasses the substantially identical DNA sequences. Preferably, the sequences used as gene probes are at least substantially identical to the corresponding native DNA sequence.

[0035] Preferred gene probes of the present invention are the DNA sequences listed in the sequence protocol, their complementary sequences or their corresponding native DNA segment.

[0036] The DNA sequences used as gene probes in present invention may also be deletion or addition mutants of the corresponding native DNA segments. In case of deletion mutants, the minimum length of the DNA sequences suitable as probes in present invention is 100 nt. Preferably, the deletions take place at the 5' - and/or 3' -terminus of the native DNA segment. In case of addition mutants, the added nucleotides may sum up to a total of 90% of the nucleotide number of the native DNA segment, if added at the 5' - or 3' - terminus of the DNA sequence. Alternatively, the additions and deletions may be of one isolated nucleotide or of 2 or more consecutive nucleotides at one or more internal site(s) of the native DNA segment. Preferably, 0-30% nucleotides of the corresponding native DNA segment are added or deleted. It is most preferred that the addition or deletion mutants used as gene probes in present invention comprise one or more segment(s) of at least 100 consecutive nt each, which are derived from one gene, and/or sequences homologous (70% homology) or complementary thereto. These segments may be embedded in or fused to other DNA sequences, which will not hybridize under stringent conditions with either human or bacterial DNA or the DNA of the target microorganism. Said other DNA sequences preferably have a maximum length which adds up with the length of the enclosed segment (s) to not more than the upper limit for the length of gene probes suitable for present invention.

[0037] A "positive blood culture" is an *in vitro* culture started from whole blood or blood components wherein the growth of microorganisms has been detected. Said growth is indicated by a positive growth index. The detection is preferably done by monitoring CO₂ production in the blood culture.

[0038] "Direct identification" of microorganisms refers to an identification method which comprises isolation of DNA from a sample or clinical specimen, but does not require an amplification of the genetic material of the microorganisms after said isolation in order to identify the microorganisms using the method of present invention. The isolated genetic material is labelled and applied to the DNA microarray of present invention without prior amplification, i.e. directly after isolation or after a short workup step.

[0039] A "detection method" in the context of the present invention is a method for determination of hybridisation of DNA molecules contained in a sample to the probes on the solid support of the microarray of present invention. This method may be any textbook method for detection of DNA hybridisation on microarrays, e.g. direct detection or labelling of target DNA with a reporter molecule and consecutive visualisation of the reporter molecule. Preferred detection methods are said labelling method and the direct detection by electrical biosensors or mass spectrometry (Liu, R. H. et al., Anal. Chem. 76(7):1824-31 (2004); Stomakhin, A. A. et al., Nucleic Acids Res. 28(5):1193-8 (2000)).

[0040] A "reporter molecule" in the context of the method of the present invention is a chemical or physical marker which allows differentiation of labelled from unlabelled DNA by physical, chemical or immunological methods. The labelling method includes, but is not limited to radioactive labelling (e.g. with ³³P, ³²P), fluorescent/luminescent/chromophor labelling and hapten labelling (i.e. psoralen or DIG). It is followed by an appropriate detection step necessary to

determine the presence and/or quantity of the reporter molecule, namely scintillation counting (e.g. phosphoimaging); photoptic measurement (e.g. fluorescence measurement, luminescence measurement) and antibody-based detection (including colorimetric, luminescence or fluorescence detection), respectively. Preferably, the reporter molecule is a fluorochrome/fluorophor (both terms are used as synonyms in the context of present invention) which includes but is not limited to cyanines, fluoresceins and rhodamines. More preferably, it is of the cyanine group of fluorophores. Most preferably, it is selected from the group consisting of the fluorophores Cy3, Cy5 or Alexa Fluor 647 and Alexa Fluor 546. The ratio of base to dye molecules (BDR) in DNA labelled with such reporter molecules is preferably less or equal to 60.

Detailed description of the invention

[0041] The present invention provides a DNA microarray and its use for rapid identification and characterisation of microorganisms in a sample or clinical specimen (embodiments (1) to (3)).

[0042] The DNA microarray of embodiment (1) of the invention comprises gene specific DNA sequences as capture probes, which allow the identification of microbial species ("target species"), especially of bacterial and fungal species, and/or their further characterisation with regard to antibiotic resistance and virulence. Preferably, it allows the identification and characterisation of the target species. It is specific, applicable to the analysis of DNA isolated from blood cultures and suitable to detect resistance genes.

[0043] One important feature of the microarray of the present invention is that the panel of probes can be continually extended to include sequences for additional species, variant isolates or antibiotic resistance determinants as they are characterised and available. The accuracy, range and discriminatory power of the gene-segment based microarray can be refined by adding or removing gene probes to the panel without significantly increasing complexity or costs. In a pilot study, three important species causing bacteremia were selected to provide a proof of principle (examples 1-10). The range of organisms that can be identified can be easily expanded by increasing the number of gene probes on the array. For example, addition of a few probes specific for *S. epidermidis* and other CoNS will allow for the species identification of coagulase-negative staphylococci. Furthermore, due to a specific hybridisation pattern for each species it will also allow the identification of mixed blood cultures with more than one pathogen.

[0044] A second important feature of this microarray format is the length of the DNA sequences used as gene probes. They are at least 100 nt, preferably 100-3000 nt long. In an especially preferred aspect of embodiment (1) the length of the gene probes is from 100 to 1000 nt, most preferably from 200 to 800 nt. Thus, one probe per gene is usually sufficient to produce strong signals and high specificity (Stears, R.L. et al., Nat. Med., 9:140-5 (2003)). For long probes like these, minor point mutations are likely to only slightly reduce duplex formation, which does not lead to the loss of hybridisation signals. In contrast, short oligonucleotide microarrays sometimes lack specificity and require multiple short oligonucleotides per one gene.

[0045] The microorganisms or microbial DNA to be detected using the microarray of present invention are preferably bacteria (such as *Staphylococci*, *Enterococci*, *Streptococci*, *E. coli*, *P. aeruginosa*) or fungi (such as yeasts and filamentous fungi, in particular *Candida* spp., *Aspergillus* spp., *Cryptococcus* spp., *Malassezia* spp., *Trichosporin* spp.), respectively bacterial or fungal DNA. The microarray is especially suitable for direct identification and characterisation of bacteria and *C. albicans*.

[0046] In one preferred aspect of embodiments (1), (2) and (3), the DNA microarray is feasible to identify and characterize any of the microorganisms, including the fungi and bacteria as defined above, known as etiological agents of fungemia, bacteremia or sepsis. In another preferred aspect of (1), it is feasible to characterize the bacteria known as etiological agents of bacteremia or sepsis. More preferably, it is feasible to identify and characterize at least 90 % of said microorganisms or bacteria. Equally more preferably it is feasible to identify and characterize microorganisms selected from the group consisting of *S. aureus*, *Coagulase-negative staphylococci*, *Enterococci*, *Streptococci*, *E. coli*, *Klebsiella* spp., *Proteus* spp., *Enterobacter* spp., *P. aeruginosa*, *Stenotrophomonas* spp., *Acinetobacter* spp. and *Candida albicans*, most preferably microorganisms selected from the group consisting of *C. albicans*, *Enterococcus faecalis*, *Enterococcus faecium*, *E. coli*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Proteus vulgaris*, *Enterobacter cloacae*, *P. aeruginosa*, *Stenotrophomonas maltophilia*, *Acinetobacter baumannii*, *S. aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus lugdunensis*, *Staphylococcus warneri*, *Streptococcus agalactiae*, *Streptococcus bovis*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*. Most preferably, it is feasible to identify and characterize at least *S. aureus*, *E. coli* and *P. aeruginosa*.

[0047] The practicability and specificity of the DNA microarray for the identification and characterisation of *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* grown in blood culture specimens was evaluated with clinical isolates and positive blood cultures (Examples 1-10). Especially preferred is a microarray which allows identification and characterisation of *S. aureus*. The latter microarray allows the detection of every *S. aureus* isolate, unambiguously identifies most of important virulence genes such as *tsst-1*, *sea*, *seb*, *eta* and antibiotic resistance genes such as *mecA*, *aacA-aphD*, *blaZ*, *ermA* and specifically distinguishes *S. aureus* from unrelated gram negative bacteria, e.g.

Escherichia coli or *Pseudomonas aeruginosa*, as well as from closely related CoNS (Example 11, Fig. 2-6).

[0048] In another preferred aspect of the invention, the microarray of (1) is suitable for diagnosis of fungemia, bacteremia or sepsis; especially for diagnosis of bacteremia, candidemia, and bacterial or *Candida* sepsis.

[0049] The present invention provides a novel approach for detection of microorganisms, especially of bacteria and fungi, by microarrays: using gene-segments it allows species identification by probing a large and diverse set of species-specific genes. Such an approach is reliable since it makes possible to identify a pathogen even when some genes have been deleted from its genome. Furthermore, the selected DNA probes are at least 100 nt, preferably 200 to 800 nt long and are therefore not sensitive to single nucleotide polymorphisms or CG-content variations in the targets. Therefore, a gene segment array according to present invention is useful for indicating the presence of a gene even though the sequence may be slightly altered e.g. by point mutations (Southern, E. et al., Nat. Genet. 21 :5-9 (1999)). Additionally, it permits species virulence and antibiotics resistance profiling all together in a single-step test. Thus, present invention provides for a significant improvement compared to the classical approach focused on the detection of a short evolutionary conserved sequence like 16S RNA.

[0050] The number and perfect composition of gene-segments necessary for a correct species identification, virulence determination and resistance profiling must be determined by empiric specificity tests. Thus, in a preferred aspect of the invention, the DNA microarray of embodiment (1) comprises the minimal number of species specific gene probes which is sufficient for species identification, the minimal number of virulence gene probes which is sufficient for virulence determination, and/or the minimal number of resistance gene probes which is sufficient for determination of resistance of a specific microorganism. Preferably, the minimal number of gene probes in this aspect of the invention is: for correct species identification at least 2 different species specific gene probes per target species, more preferably at least 10, most preferably at least 20; for virulence determination at least 1 gene probe per target species, more preferably at least 5 different gene probes, even more preferably at least 20 different gene probes, most preferably gene probes for all known virulence factors of each target species; for determination of resistance at least 1 gene probe per antibiotic class or resistance factor, more preferably at least 5 different gene probes, most preferably all known gene-coded resistance determinants in the target species.

[0051] Generally, the DNA microarray of embodiment (1) comprises gene probes which are specific for a microbial species, bacterial/fungal species or a group of microorganisms to be identified. Said gene probes are preferably DNA sequences selected from three different groups, namely (a) species specific gene probes; (b) virulence gene probes; and/or (c) resistance gene probes. Preferably, the species specific set of gene probes for each species to be identified and characterised is selected from species specific gene probes (a) for

(i) *Staphylococcus aureus* including gene probes derived from *cataSaur*, *clfA*, *clfB*, *coa*, *l-clpC*, *l-clpP*, *l-ctaA*, *l-ctsR*, *l-dltA*, *l-dltB*, *l-dltC*, *l-dnaK*, *l-elkT*, *l-femD*, *l-glnA*, *l-glnR*, *l-grlA*, *l-grlB*, *l-groEL*, *l-groES*, *l-hemA*, *l-hemE*, *l-hemH*, *l-hemL*, *l-hemY*, *l-lepA*, *l-lrgA*, *l-lrgB*, *l-lytM*, *l-menB*, *l-menD*, *l-menE*, *l-menF*, *l-mreB*, *l-mreR*, *l-mutL*, *l-mutS*, *l-NAG*, *l-pbg*, *l-pbpF*, *l-pdhB*, *l-pdhC*, *l-rsbU*, *l-rsbV*, *l-rsbW*, *l-sgp*, *l-sirR*, *l-sodA*, *l-sodB*, *l-sstA*, *l-sstB*, *l-sstC*, *l-sstD*, *l-trx*, *l-yhiN*, *epiP-bsaP*, *geh*, *gyrA*, *gyrB*, *hemB*, *hemC*, *hemD*, *hemN*, *hsdS*, *lip*, *menC*, *nuc*, *pdhD*, *rpoB*, *SAV0431*, *SAV0439*, *SAV0440*, *SAV0441*, *sigB*, *spa*, *sstC*, *tag*, *tyrA*, *l-aroC*, *l-aroA*, *l-cna*, *l-ebpS*, *l-eno*, *l-fbpA*, *l-fib*, *l-fnbB*, *l-srtA*, *l-stpC*, *l-fnbA*, *l-spa*, *l-aroE*, *l-aroF*, *l-aroG*, *l-asp23*, *l-atl*;

(ii) *Escherichia coli* including gene probes derived from *b1169*, *envZ*, *fliCb*, *nfrB*, *nlpA*, *pilAe*, *yacH*, *yagX*, *ycdS*, *yciQ*, *ymcA*;

(iii) *Staphylococcus epidermidis* including gene probes derived from *ardeSE0106*, *ardeSE0107*, *aroSE0105*, *atlE*, *agrB*, *agrC*, *alphSE1368*, *gad*, *glucSE1191*, *hsp10*, *icaA*, *icaB*, *m vaSSepid*, *nitreSE1972*, *nitreSE1974*, *nitreSE1975*, *oiamtSE1209*, *ORF1Sepid*, *ORF3bSepid*, *qacR*, *sin*, *ureSE1861*, *ureSE1863*, *ureSE1864*, *ureSE1865*, *ureSE1867*;

(iv) *Staphylococcus haemolyticus* including gene probes derived from *folQShaemolyt*, *mvaCShaemolyticus*, *mvaD-Shaemolyt*, *mvaK1Shaemolyticus*, *mvaSShaemolyticus*, *RNApolsigm*;

(v) *Staphylococcus lugdunensis* including gene probes derived from *agrB2Stalugd*, *agrC2Stalugd*, *agrCStalugd*, *slamStalugd*;

(vi) *Staphylococcus warneri* including gene probes derived from *msrw1Stwar*, *nukMStwar*, *proDStwar*, *proMStwar*, *sigrpoStwar*, *tnpStwar*;

(vii) *Candida albicans* including gene probes derived from *ARG56*, *ASL43f*, *BGL2*, *CACHS3*, *CCT8*, *CDC37*, *CEF3*, *CHS1*, *CHS2*, *CHS4*, *CHS5*, *CHT1*, *CHT2*, *CHT4*, *CSA1*, *5triphosphatase*, *AAF1*, *ADH1*, *ALS1*, *ALS7*, *EDT1*, *ELF*, *ESS1*, *FAL1*, *GAP1*, *GNA1*, *GSC1*, *GSL1*, *HIS1*, *HTS1*, *HWP1*, *HYR1*, *INT1a*, *KRE15f*, *KRE6*, *KRE9*, *MIG1*, *MLS1*, *MP65*, *NDE1*, *PFK2*, *PHR1*, *PHR2*, *PHR3*, *PRA1*, *PRS1*, *RBT1*, *RBT4*, *RHO1*, *RNR1*, *RPB7*, *RPL13*, *RVS167*, *SHA3*, *SKN1*, *SRB1*, *TCA1*, *TRP1*, *YAE1*, *YRB1*, *YST1exon2*;

(viii) *Enterococcus faecalis* including gene probes derived from *arcA*, *arcC*, *bkdA*, *cad*, *camE1*, *csrA*, *dacA*, *dfr*, *dhoD1a*, *ABC-eltA*, *agrBfs*, *agrCfs*, *dnaE*, *ebsA*, *ebsB*, *eep*, *efaR*, *gls24_glsB*, *gph*, *gyrAEf*, *metEf*, *mntHCb2*, *mob2*, *mvaD*, *mvaE*, *parC*, *pcfG*, *phoZ*, *polC*, *ptb*, *recS1*, *rpoN*, *tms*, *tyrDC*, *tyrs*;

(ix) *Enterococcus faecium* including gene probes derived from *bglB*, *bglR*, *bglS*, *efmA*, *efmB*, *efmC*, *mreC*, *mreD*, *mvaDEfaecium*, *mvaEEfaecium*, *mvaK1Efaecium*, *mvaK2Efaecium*, *mvaSEfaecium*, *orf3_4Efaecium*, *orf6_7Efaecium*, *orf7_8Efaecium*, *orf9_10Efaecium*;

(x) *Klebsiella pneumonia* including gene probes derived from *atsA*, *atsB*, *budC*, *citA*, *citW*, *citX*, *dalD*, *dalK*, *dalT*, *acoA*, *acoB*, *acoC*, *ahfK*, *fimK*, *glfKPN2*, *ltrA*, *mdcC*, *mdcF*, *mdcH*, *mrkA*, *mtrK*, *nifF*, *nifK*, *nifN*, *tyrP*, *ureA*, *wbbO*, *wza*, *wzb*, *wzmKPN2*, *wztKPN2*, *yohH*, *liac*;

(xi) *Klebsiella oxytoca* including gene probes derived from *cymA*, *cymD*, *cymE*, *cymH*, *cymI*, *cymJ*, *ddrA*, *fdt-1*, *fdt-2*, *fdt-3*, *gatY*, *hydH*, *masA*, *nasA*, *nasE*, *nasF*, *pehX*, *pelX*, *tagH*, *tagK*, *tagT*;

(xii) *Pseudomonas aeruginosa* including gene probes derived from *glpR*, *lasRb*, *OrfX*, *pa0260*, *pa0572*, *pa0625*, *pa0636*, *pa1046*, *pa1069*, *pa1846*, *pa3866*, *pa4082*, *pilAp*, *PilAp2*, *pilC*, *PstP*, *purK*, *uvrDII*, *vsml*, *vsmR*, *xcpX*;

(xiii) *Streptococcus pneumoniae* including gene probes derived from *cap1EStrepneu*, *cap1FStrepneu*, *cap1GStrepneu*, *cap3AStrepneu*, *cap3BStrepneu*, *celAStrepneu*, *celBStrepneu*, *cglAStrepneu*, *cglBStrepneu*, *cglCStrepneu*, *cglDStrepneu*, *cinA*, *cps14EStrepneu*, *cps14FStrepneu*, *cps14GStrepneu*, *cps14HStrepneu*, *cps19aHStrepneu*, *cps19aKStrepneu*, *cps19aLStrepneu*, *cps19fGStrepneu*, *cps23fGStrepneu*, *dexB*, *dinF*, *1760Strepneu*, *acyPStrepneu*, *endAStrepneu*, *exoAStrepneu*, *exp72*, *fnlAStrepneu*, *fnlBStrepneu*, *fnlCStrepneu*, *gct18Strepneu*, *hexB1*, *hftsHStrepneu*, *immunofrag1Strepneu*, *immunofrag2Strepneu*, *immunofrag3Strepneu*, *KdtBStrepneu*, *lyAStrepneu*, *pcpBStrepneu*, *pflCStrepneu*, *plpA*, *prtA1Strepneu*, *pspC1Strepneu*, *pspC2*, *purRStrepneu*, *pyrDAStrepneu*, *SP0828Strepneu*, *SP0830Strepneu*, *SP0833Strepneu*, *SP0837_38Strepneu*, *SP0839Strepneu*, *ugdStrepneu*, *uncC*, *vicXStrepneu*, *wchA6bStrepneu*, *wci4Strepneu*, *wciK4Strepneu*, *wciL4Strepneu*, *wciN6bStrepneu*, *wciO6bStrepneu*, *wciP6bStrepneu*, *wciY18Strepneu*, *wzdbStrepneu*, *wze6bStrepneu*, *wzy18Strepneu*, *wzy4Strepneu*, *wzy6bStrepneu*, *xpt*;

(xiv) *Streptococcus agalactiae* including gene probes derived from *cpsA1Strgal*, *cpsB1Strgal*, *cpsC1Strgal*, *cpsD1Strgal*, *cpsE1Strgal*, *cpsG1Strgal*, *cpsI1Strgal*, *cpsJ1Strgal*, *cpsK1Strgal*, *cpsM1Strgal*, *cpsY1Strgal*, *cylBStraga*, *cylE1Straga*, *cylF1Straga*, *cylH1Straga*, *cylI1Straga*, *cylJ1Straga*, *cylK1Straga*, *0487Straga*, *0488Straga*, *0493Straga*, *0495Straga*, *0498Straga*, *0500Straga*, *0502Straga*, *0504Straga*, *folDStraga*, *neuA1Strgal*, *neuB1Strgal*, *neuC1Strgal*, *neuD1Strgal*, *recN1Straga*, *ileS1Straga*;

(xv) *Streptococcus pyogenes* including gene probes derived from *cyclStrpyog*, *fah_rph_hlo_Strpyog*, *int*, *int315.5*, *murE1Strpyog*, *oppA*, *oppC1Strpyog*, *oppD*, *SPy0382Strpyog*, *SPy0390Strpyog*, *SPyM3_1351*, *vicX1Strpyog*;

(xvi) *Streptococcus viridans* including gene probes derived from *573Strpmut*, *580SStrpmut*, *581_582SStrpmut*, *584SStrpmut*, *dltA1Strmut*, *dltB1Strmut*, *dltC1Strmut*, *dltD1Strmut*, *lich1Strmut*, *lytR1Strmut*, *lytS1Strmut*, *pepQ1Strmut*, *pflC1Strmut*, *recN1Strmut*, *ytqB1Strmut*;

(xvii) *Proteus mirabilis* including gene probes derived from *atfA*, *atfB*, *atfC*, *ccmPrmi1*, *cyaPrmi*, *aad*, *flfB*, *flfD*, *flfN*, *flhD*, *floA*, *ftsK*, *gstB*, *hemCPrmi*, *hemDPrmi*, *hev*, *katA*, *lpp1*, *menE*, *mfd*, *nrpA*, *nrpB*, *nrpG*, *nrpS*, *nrpT*, *nrpU*, *pat*, *pmfA*, *pmfC*, *pmfE*, *ppaA*, *rsbA*, *rsbC*, *speB*, *stmA*, *stmB*, *terA*, *terD*, *umoA*, *umoB*, *umoC*, *ureR*, *xerC*, *ygbA*;

(xviii) *Proteus vulgaris* including gene probes derived from *envZPrvu*, *frdC*, *frdD*, *infBPrvu*, *lad*, *tna2*.

[0052] Preferably, the virulence specific set of gene probes for each species to be identified and characterised is selected from virulence gene probes (b) for

(i) *Staphylococcus aureus* including gene probes derived from *bsaE*, *bsaG*, *cap5h*, *cap5i*, *cap5j*, *cap5k*, *cap8H*, *cap8I*, *cap8J*, *cap8K*, *I-hld*, *I-hysA*, *I-IgGbg*, *EDIN*, *eta*, *etb*, *hglA*, *hglB*, *hglC*, *hla*, *hlyB*, *lukF*, *lukS*, *NAG*, *sak*, *sea*, *seb*, *sec1*, *seg*, *seh*, *sel*, *set15*, *set6*, *set7*, *set8*, *sprV8*, *tst*, *I-sdrC*, *I-sdrD*, *I-sdrE*;

(ii) *Escherichia coli* including gene probes derived from *b1202*, *eae*, *eltB*, *escR*, *escT*, *escU*, *espB*, *fes*, *fteA*, *hlyA*, *hlyB*, *iucA*, *iucB*, *iucC*, *papG*, *rfaE*, *shuA*, *SLTII*, *toxALTPA*, *VT2vaB*;

(iii) *Staphylococcus epidermidis* including gene probes derived from *gcaD*, *hld_orf5*, *icaC*, *icaD*, *icaR*, *psm_beta1and2*, *purR*, *spoVG*, *yabJ*;

(iv) *Staphylococcus haemolyticus* including gene probes derived from *lipShaemolyt*;

(v) *Staphylococcus lugdunensis* including gene probes derived from *fblStalugd*, *slushABCStalugd*;

(vi) *Staphylococcus warneri* including gene probes derived from *gehAStwar*;

(vii) *Candida albicans* including gene probes derived from *CCN1*, *CDC28*, *CLN2*, *CPH1*, *CYB1*, *EFG1*, *MNT1*, *RBF1*, *RBF1*, *RIM101*, *RIM8*, *SEC14*, *SEC4*, *TUP1*, *YPT1*, *ZNF1* *CZF1*;

(viii) *Enterococcus faecalis* including gene probes derived from *asa1*, *asp1*, *cgh*, *cylA*, *cylB*, *cyll*, *cyll_cylS*, *cyllM*, *ace*, *ef00108*, *ef00109*, *ef00111*, *ef00113*, *ef00112*, *ef0022*, *ef0031*, *ef0032*, *ef0040*, *ef0058*, *enlA*, *esa*, *esp*, *gelE*, *groEL*, *groES*, *rt1*, *sala*, *salb*, *sea1*, *sep1*, *vicK*, *yyhH*, *yycl*, *yycJ*;

(ix) *Enterococcus faecium* including gene probes derived from *entA_entl*, *entD*, *entR*, *oep*, *sagA*;

(x) *Klebsiella pneumonia* including gene probes derived from *cim*, *aldA*, *hemly*, *pSL017*, *pSL020*, *rcaA*, *rmlC*, *rmlD*, *waaG*, *wbbD*, *wbbM*, *wbbN*, *wbdA*, *wbdC*, *wztKpn*, *yibD*;

(xi) *P. aeruginosa* including gene probes derived from *aprA*, *aprE*, *ctx*, *algB*, *algN*, *algR*, *ExoS*, *fpvA*, *lasRa*, *lipA*,

lipH, *Orf159*, *Orf252*, *pchG*, *PhzA*, *PhzB*, *PLC*, *plcN*, *plcR*, *pvdD*, *pvdF*, *pyocinS1*, *pyocinS1im*, *pyocinS2*, *pys2*, *rbf303*, *rhlA*, *rhlB*, *rhlR*, *TnAP41*, *toxA*;

(xii) *Streptococcus pneumoniae* including gene probes derived from *igaStrpneu*, *lytA*, *nanA*, *nanBStrpneu*, *pcpC-Strpneu*, *ply*, *prtAStrpneu*, *pspA*, *SP0834Strpneu*, *sphtraStrpneu*, *wciJStrpneu*, *wziyStrpneu*, *wzxStrpneu*;

(xiii) *Streptococcus agalactiae* including gene probes derived from *CAMPfactor*, *0499Straga*, *hylStragal*, *lipStragal*;

(xiv) *Streptococcus pyogenes* including gene probes derived from *DNaseIStropyog*, *fba2Stropyog*, *fhuAStropyog*, *fhuB1Stropyog*, *fhuDStropyog*, *fhuGStropyog*, *hylA*, *hylP*, *hylp2*, *oppB*, *ropB*, *scpAStropyog*, *sloStropyog*, *smez-Strpyog*, *sof*, *speA*, *speB2Stropyog*, *speCStropyog*, *speJStropyog*, *srtBStropyog*, *srtCStropyog*, *srtEStropyog*, *srtFStropyog*, *srtGStropyog*, *srtIStropyog*, *srtKStropyog*, *srtRStropyog*, *srtTStropyog*, *vicKStropyog*;

(xvi) *Streptococcus viridans* including gene probes derived from *hlyXStrmut*, *igaStrmitis*, *igaStrsanguis*, *perMStrmut*;

(xvii) *Proteus mirabilis* including gene probes derived from *flaA*, *laD*, *fliA*, *hpmA*, *hpmB*, *lpsPrmi*, *mrpA*, *mrpB*, *mrpC*, *mrpD*, *mrpE*, *mrpF*, *mrpG*, *mrpH*, *mrpI*, *mrpJ*, *patA*, *putA*, *uca*, *ureDPrmi*, *ureEPrmi*, *ureFPrmi*, *zapA*, *zapB*, *zapD*, *zapE*.

[0053] Preferably, the resistance specific set of gene probes is selected from resistance gene probes (c) derived from genes coding for

(i) beta-lactams resistance including gene probes derived from *blaIMP-7*, *meclSepid*, *blaOXA-10*, *blaB*, *ampC*, *I-blaR*, *blaOXA-32*, *bla-CTX-M-22*, *pbp2aStrpneu*, *blaSHV-1*, *blaOXA-2*, *blaRShaemolyt*, *blaIMP-7*, *I-mecR*, *blaOXY*, *dacCStropyog*, *femA*, *mecA*, *blaShaemolyt*, *blavim*, *pbp2b*, *pbp2prim*, *eSepid*, *pbp2x*, *pbp3Saureuc*, *pbp4*, *pbp5Efaecium*, *pbpC*, *I-mecI*, *pbp1a*, *I-blaI*, *blaTEM-106*, *blaOXY-KLOX*, *ftsWEF*, *fmhB*, *cumA*, *femBShaemolyt*, *blaPER-1*, *bla_FOX-3*, *blaA*, *psrb*, *fmhA*, *mecR1Sepid*, *blaZ*, *blaOXA-1*, *fox-6*, *blaPrmi*;

(ii) aminoglycosides resistance including gene probes derived from *aacA_aphDStwar*, *aacC1*, *aacC2*, *strB*, *aadA*, *aadB*, *aadD*, *aacA4*, *strA*, *aph-A3*, *aacC1*, *aacA4*, *aacA-aphD*, *I-spc*, *aphA3*;

(iii) macrolides-lincosamines-streptogramins resistance including gene probes derived from *ermC*, *linB*, *satSA*, *mdrSA*, *I-linA*, *ermB*, *ermA*, *sata*, *msrA*, *mphBM*, *mefA*, *mrx*;

(iv) trim ethoprim resistance including gene probes derived from *dfrA*, *dfrStrpneu*;

(v) chloramphenicol resistance including gene probes derived from *cat*, *catEfaecium*, *cmlA5*;

(vi) tetracyclines resistance including gene probes derived from *tetAJ*, *tetL*, *tetM*

(vii) glycopeptides resistance including gene probes derived from *vanH(tn)*, *vanA*, *vanHB2*, *vanR*, *vanRB2*, *vanS(tn)*, *vanSB2*, *vanVIIb2*, *ddl*, *ble*, *vanXB2*, *vanY(tn)*, *vanYB2*, *vanB*, *vanZ(tn)*, *vanC-2*, *vanX(tn)*;

(viii) multiple target resistance including gene probes derived from *acrB*, *m exB*, *I-qacA*, *sull*, *sul*, *cadBStalugd*, *mexA*, *acrR*, *emeA*, *acrA*, *rtn*, *abcXStrpmut*, *qacEdelta1*, *elkT-abcA*, *1-cadA*, *albA*, *wzm*, *msrCb*, *nov*, *wzt*, *wbbI*, *norA23*, *mexR*, *arr2*, *mreA*, *I-cadC*, *uvrA*;

(ix) fungicides resistance, especially *C. albicans* fungicide resistance, including gene probes derived from *CRD2*, *CDR1*, *MET3*, *FET3*, *FTR2*, *MDR1-7*, *ERG11*, *SEC20*.

[0054] Furthermore, the microarray may contain a set of gene probes which serve as controls. Preferably, such a set of control gene probes is selected from group (d) consisting of control gene probes coding for

(i) negative controls, namely DNA sequences which will not hybridise with human DNA or bacterial, fungal or the microbial target DNA under the hybridisation conditions of the method of present invention, including gene probes derived neither from fungal, bacterial or target microbial nor from human genes, preferably gene probes derived from plant genes, more preferably from *Arabidopsis thaliana* or *Glycine max* genes;

(ii) positive controls including segments of ribosomal DNA from bacterial target species, preferably 16S DNA, and segments of conserved human genes;

(iii) positive controls specific for DNA added to the sample ("spiked DNA"), namely DNA sequences which will not hybridise with human DNA or the fungal, bacterial or microbial target DNA under the hybridisation conditions of the method of present invention, including gene probes derived neither from fungal, bacterial or target microbial nor from human genes, preferably gene probes derived from mouse or amoeba genes, most preferably from *Mus musculus* or *Dictyostelium discoideum* genes.

[0055] These control gene probes are necessary to

- detect non-specific hybridisation;
- optimise hybridisation conditions and image acquisition and analysis;
- provide positive controls for the quality of probe preparation, hybridisation and detection; and/or
- control technical aspects of the entire detection procedure including labelling, hybridisation and detection steps.

[0056] In a preferred aspect of embodiment (1), the microarray contains DNA sequences selected from the group consisting of the SEQ ID NOs: 1-918, complementary sequences thereto, addition mutants, deletion mutants, substitution mutants and homologues thereof as gene probes.

[0057] More preferably, in order to identify a specific microbial species, bacterial species or group of bacteria, the gene probes of group (a) are selected from SEQ ID NO: 1-99, 142-152, 174-199, 209-214, 216-219, 222-229, 231-291, 308-342, 377-393, 399-431, 449-490, 523-591, 606-639, 645-656, 687-701, 706-749 and 776-781 (compare Tab. 1). Equally, in order to determine virulence of a specific microorganism or bacterial species, the gene probes of group (b) are selected from SEQ ID NO: 100-141, 153-173, 200-208, 215, 220-221, 230, 292-307, 343-376, 394-398, 432-448, 491-522, 592-605, 640-644, 657-686, 702-705, 750-775 and 782-784 (compare Tab. 1). Equally, in order to determine antibiotic resistance of a specific microbial or bacterial species, the gene probes of group (c) are selected from SEQ ID NO: 785-918, preferably from SEQ ID NO: 785-882 (compare Tab. 1). Equally, in order to provide the required controls (negative, positive, hybridisation controls), the gene probes of group (d) are selected from SEQ ID NO: 919-947, preferably from SEQ ID NO: 919-925 and 944-947, more preferably from SEQ ID NO: 919 and 921 (compare Tab. 1).

[0058] Tab. 1: Preferred gene probes for species identification, virulence determination and resistance determination of microorganisms

a) probes for species identification

SEQ ID NO	Probe
<i>Staphylococcus aureus</i> identification	
1	cataSaur_1_1
2	cataSaur_1_2
3	clfA_1_1
4	clfB_1_1
5	coa_1_1
6	coa_1_2
7	l-clpC_1_1
8	l-clpP_1_1
9	l-ctaA_1_1
10	l-ctsR_1_1
11	l-dltA_1_1
12	l-dltB_1_1
13	l-dltC_1_1
14	l-dnaK_1_1
15	l-elkT_1_1
16	l-femD_1_1
17	l-glnA_1_1
18	l-glnR_1_1
19	l-qrIA_1_1
20	l-grlB_1_1
21	l-groEL_1_1
22	l-groES_1_1
23	l-hemA_1_1
24	l-hemE_1_1
25	l-hemH_1_1
26	l-hemL_1_1

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(continued)

SEQ ID NO	Probe
<i>Staphylococcus aureus</i> identification	
27	I-hemY_1_1
28	I-lepA_1_1
29	I-lrgA_1_1
30	I-lrgB_1_1
31	I-lytM_1_1
32	I-menB_1_1
33	I-menD_1_1
34	I-menE_1_1
35	I-menF_1_1
36	I-mreB_1_1
37	I-mreR_1_1
38	I-mutL_1_1
39	I-mutS_1_1
40	I-NAG_1_1
41	I-pbg_1_1
42	I-pbpF_1_1
43	I-pdhB_1_1
44	I-pdhC_1_1
45	I-rsbU_1_1
46	I-rsbV_1_1
47	I-rsbW_1_1
48	I-sgp_1_1
49	I-sirR_1_1
50	I-sodA_1_1
51	I-sodB_1_1
52	I-sstA_1_1
53	I-sstB_1_1
54	I-sstC_1_1
55	I-sstD_1_1
56	I-trx_1_1
57	I-yhiN_1_1
58	epiP-bsaP_1_1
59	geh_1_1
60	gyrA_1_1
61	gyrB_1_1
62	hemB_1_1
63	hemC_1_1

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SEQ ID NO	Probe
<i>Staphylococcus aureus</i> identification	
64	hemD_1_1
65	hemN_1_1
66	hsdS_1_1
67	hsdS_2_1
68	lip_1_1
69	menC_1_1
70	murC_1_1
71	nuc_1_1
72	pdhD_1_1
73	rpoB_1_1
74	SAV0431_1_1
75	SAV0439_1_1
76	SAV0440_1_1
77	SAV0441_1_1
78	sigB_1_1
79	spa_1_2
80	sstC_1_1
81	tag_1_1
82	tyrA_1_1
83	l-aroC_1_1
84	l-aroA_1_1
85	l-cna_1_1
86	l-ebpS_1_1
87	l-eno_1_1
88	l-fbpA_1_1
89	l-fib_1_1
90	l-fnbB_1_1
91	l-srtA_1_1
92	l-stpC_1_1
93	l-fnbA_1_1
94	l-spa_1_1
95	l-aroE_1_1
96	l-aroF_1_1
97	l-aroG_1_1
98	l-asp23_1_1
99	l-atl_1_1

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(continued)

<i>Escherichia coli</i> identification	
142	b1169_1_1
143	envZ_1_1
144	fliCb_1_1
145	nfrB_1_1
146	nlpA_1_1
147	piIAe_1_1
148	yacH_1_1
149	yagX_1_1
150	ycdS_1_1
151	yciQ_1_1
152	ymcA_1_1
<i>Staphylococcus epidermidis</i> identification	
174	ardeSE0106_1_1
175	ardeSE0107_1_1
176	aroiSE0105_1_1
177	atlE_1_1
178	agrB_1_1
179	agrC_1_1
180	alphSE1368_1_1
181	gad_1_1
182	glucSE1191_1_1
183	hspI0_1_1
184	icaA_1_1
185	icaB_1_1
186	mvaSSepid_1_1
187	nitreSE1972_1_1
188	nitreSE1974_1_1
189	nitreSE1975_1_1
190	oiamtSE1209_1_1
191	ORF1Sepid_1_1
192	ORF3bSepid_1_1
193	qacR_1_1
194	sin_1_1
195	ureSE1861_1_1
196	ureSE1863_1_1
197	ureSE1864_1_1
198	ureSE1865_1_1

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<i>Staphylococcus epidermidis</i> identification	
199	ureSE1867_1_1
<i>Staphylococcus haemolyticus</i> identification	
209	folQShaemolyt_1_1
210	mvaCShaemolyticus_1_1
211	mvaDShaemolyt_1_1
212	mvaK1 Shaemolyticus_1_1
213	mvaSShaemolyticus_1_1
214	RNApolsigm_1_1
<i>Staphylococcus lugdunensis</i> identification	
216	agrB2Stalugd_1_1
217	agrC2Stalugd_1_1
218	agrCStalugd_1_1
219	slamStalugd_1_1
<i>Staphylococcus saprophyticus</i> identification	
222	RNApolsigmSsapro_1_1
223	RNApolsigmSsapro_1_2
<i>Staphylococcus warneri</i> identification	
224	msrw1Stwar_1_1
225	nukMStwar_1_1
226	proDStwar_1_1
227	proMStwar_1_1
228	sigrpoStwar_1_1
229	tnpStwar_1_1
<i>Candida albicans</i> identification	
231	ARG56_1_1
232	ASL43f_1_1
233	BGL2_1_1
234	CACHS3_1_1
235	CCT8_1_1
236	CDC37_1_1
237	CEF3_1_1
238	CHS1_1_1
239	CHS2_1_1

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(continued)

<i>Candida albicans</i> identification	
240	CHS4_1_1
241	CHS5_1_1
242	CHT1_1_1
243	CHT2_1_1
244	CHT4_1_1
245	CSA1_1_1
246	5triphosphatase_1_1
247	AAF1_1_1
248	ADH1_1_1
249	ALS1_1_1
250	ALS7_1_1
251	EDT1_1_1
252	ELF_1_1
253	ESS1_1_1
254	FAL1_1_1
255	GAP1_1_1
256	GNA1_1_1
257	GSC1_1_1
258	GSL1_1_1
259	HIS1_1_1
260	HTS1_1_1
261	HWP1_2_1
262	HYR1_1_1
263	INT1a_1_1
264	KRE15f_1_1
265	KRE6_1_1
266	KRE9_1_1
267	MIG1_1_1
268	MLS_1_1
269	MP65_1_1
270	NDE1_1_1
271	PFK2_1_1
272	PHR1_1_1
273	PHR2_1_1
274	PHR3_1_1
275	PRA1_1_1
276	PRS_1_1
277	RBT1_1_1

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(continued)

<i>Candida albicans</i> identification	
278	RBT4_1_1
279	RHO1_1_1
280	RNR1_1_1
281	RPB7_1_1
282	RPL13_1_1
283	RVS167_1_1
284	SHA3_1_1
285	SKN1_1_1
286	SRB1_1_1
287	TCA1_1_1
288	TRP1_1_1
289	YAE1_1_1
290	YRB1_1_1
291	YST1exon2_1_1
<i>Enterococcus faecalis</i> identification	
308	arcA_1_1
309	arcC_1_1
310	bkdA_1_1
311	cad_1_1
312	camE1_1_1
313	csrA_1_1
314	dacA_1_1
315	dfr_1_1
316	dhoD1a_1_1
317	ABC-eltA_1_1
318	agrBfs_1_1
319	agrCfs_1_1
320	dnaE_1_1
321	ebsA_1_1
322	ebsB_1_1
323	eep_1_1
324	efaR_1_1
325	gls24_glsB_1_1
326	gph_1_1
327	gyrAEf_1_1
328	metEf_1_1
329	mntHCb2_1_1

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(continued)

<i>Enterococcus faecalis</i> identification	
330	mob2_1_1
331	mvaD_1_1
332	mvaE_1_1
333	parC_1_1
334	pcfG_1_1
335	phoZ_1_1
336	polC_1_1
337	ptb_1_1
338	recS1_1_1
339	rpoN_1_1
340	tms_1_1
341	tyrDC_1_1
342	tyrS_1_1
<i>Enterococcus faecium</i> identification	
377	bglB_1_1
378	bglR_1_1
379	bglS_1_1
380	efmA_1_1
381	efmB_1_1
382	efmC_1_1
383	mreC_1_1
384	mreD_1_1
385	mvaDEfaecium_1_1
386	mvaEEfaecium_1_1
387	mvaK1Efaecium_1_1
388	mvaK2Efaecium_1_1
389	mvaSEfaecium_1_1
390	orf3_4Efaeciumb_1_1
391	orf6_7Efaecium_1_1
392	orf7_8Efaecium_1_1
393	orf9_10Efaecium_1_1
<i>Klebsiella pneumoniae</i> identification	
399	atsA_1_1
400	atsB_1_1
401	budC_1_1
402	citA_1_1

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(continued)

<i>Klebsiella pneumoniae</i> identification	
403	citW_1_1
404	citX_1_1
405	dalD_1_1
406	dalK_1_1
407	dalT_1_1
408	acoA_1_1
409	acoB_1_1
410	acoC_1_1
411	ahlK_1_1
412	fimK_1_1
413	glfKPN2_1_1
414	ltrA_1_1
415	mdcC_1_1
416	mdcF_1_1
417	mdcH_1_1
418	mrkA_1_1
419	mtrK_1_1
420	nifF_1_1
421	nifK_1_1
422	nifN_1_1
423	tyrP_1_1
424	ureA_1_1
425	wbbO_1_1
426	wza_1_1
427	wzb_1_1
428	wzmKPN2_1_1
429	wztKPN2_1_1
430	yojH_1_1
431	liac_1_1
<i>Klebsiella oxytoca</i> identification	
449	cymA_1_1
450	cymD_1_1
451	cymE_1_1
452	cymH_1_1
453	cymI_1_1
454	cymJ_1_1
455	ddrA_1_1

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(continued)

<i>Klebsiella oxytoca</i> identification	
456	fdt-1_1_1
457	fdt-2_1_1
458	fdt-3_1_1
459	gatY_1_1
460	hydH_1_1
461	masA_1_1
462	nasA_1_1
463	nasE_1_1
464	nasF_1_1
465	pehX_1_1
466	pelX_1_1
467	tagH_1_1
468	tagK_1_1
469	tagT_1_1
<i>Pseudomonas aeruginosa</i> identification	
470	glpR_1_1
471	lasRb_1_1
472	OrfX_1_1
473	pa0260_1_1
474	pa0572_1_1
475	pa0625_1_1
476	pa0636_1_1
477	pa1046_1_1
478	pa1069_1_1
479	pa1846_1_1
480	pa3866_1_1
481	pa4082_1_1
482	pilAp_1_1
483	PilAp2_1_1
484	pilC_1_1
485	PstP_1_1
486	purK_1_1
487	uvrDII_1_1
488	vsml_1_1
489	vsmR_1_2
490	xcpX_1_1
<i>Streptococcus pneumoniae</i> identification	
523	cap1EStrpneu_1_1

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<i>Streptococcus pneumoniae</i> identification	
524	cap1FStrpneu_1_1
525	cap1GStrpneu_1_1
526	cap3AStrpneu_1_1
527	cap3BStrpneu_1_1
528	celAStrpneu_1_1
529	celBStrpneu_1_1
530	cglAStrpneu_1_1
531	cglBStrpneu_1_1
532	cglCStrpneu_1_1
533	cglDStrpneu_1_1
534	cinA_1_1
535	cps14EStrpneum_1_1
536	cps14FStrpneum_1_1
537	cps14GStrpneum_1_1
538	cps14HStrpneum_1_1
539	cps19aHStrpneum_1_1
540	cps19aIStrpneum_1_1
541	cps19aKStrpneum_1_1
542	cps19fGStrpneum_1_1
543	cps23fGStrpneum_1_1
544	dexB_1_1
545	dinF_1_1
546	1760Strpneu_1_1
547	acyPStrpneu_1_1
548	endAStrpneu_1_1
549	exoAStrpneu_1_1
550	exp72_1_1
551	fnIAStrpneu_1_1
552	fnIBStrpneu_1_1
553	fnICStrpneu_1_1
554	gct18Strpneum_1_1
555	hexB1_1_1
556	hftsHstrpneu_1_1
557	immunofrag1Strpneu_1_1
558	immunofrag2Strpneu_2_1
559	immunofrag3Strpneu_2_1
560	kdtBStrpneu_1_1
561	lysAStrpneu_1_1

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<i>Streptococcus pneumoniae</i> identification	
562	pcpBStrpneu_1_1
563	pflCStrpneu_1_1
564	plpA_1_1
565	prtA1Strpneu_1_1
566	pspC1Strpneu_1_1
567	pspC2_1_1
568	purRStrpneu_1_1
569	pyrDAStrpneu_1_1
570	SP0828Strpneu_1_1
571	SP0830Strpneu_1_1
572	SP0833Strpneu_1_1
573	SP0837_38Strpneu_1_1
574	SP0839Strpneu_1_1
575	ugdStrpneu_1_1
576	uncC_1_1
577	vicXStrpneu_1_1
578	wchA6bStrpneu_1_1
579	wci4Strpneu_1_1
580	wciK4Strpneu_1_1
581	wciL4Strpneu_1_1
582	wciN6bStrpneu_1_1
583	wciO6bStrpneu_1_1
584	wciP6bStrpneu_1_1
585	wciY18Strpneu_1_1
586	wzdbStrpneu_1_1
587	wze6bStrpneu_1_1
588	wzy18Strpneu_1_1
589	wzy4Strpneu_1_1
590	wzy6bStrpneu_1_1
591	xpt_1_1
<i>Streptococcus agalactiae</i> identification	
606	cpsA1Strgal_1_1
607	cpsB1Strgal_1_1
608	cpsC1Strgal_1_1
609	cpsD1Strgal_1_1
610	cpsE1Strgal_1_1
611	cpsG1Strgal_1_1
612	cpsI1Strgal_1_1

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<i>Streptococcus agalactiae</i> identification	
613	cpsJStragal_1_1
614	cpsKStragal_1_1
615	cpsMStragal_1_1
616	cpsYStragal_1_1
617	cpsYStragal_2_1
618	cylBStraga_1_1
619	cylEStraga_1_1
620	cylFStraga_1_1
621	cylHStraga_1_1
622	cylIStraga_1_1
623	cylJStraga_1_1
624	cylKStraga_1_1
625	0487Straga_1_1
626	0488Straga_1_1
627	0493Straga_1_1
628	0495Straga_1_1
629	0498Straga_1_1
630	0500Straga_1_1
631	0502Straga_1_1
632	0504Straga_1_1
633	foldStraga_1_1
634	neuA1Strgal_1_1
635	neuB1Strgal_1_1
636	neuC1Strgal_1_1
637	neuD1Strgal_1_1
638	recNStraga_1_1
639	ileSStraga_1_1
<i>Streptococcus pyogenes</i> identification	
645	cyclStrpyog_1_1
646	fah_rph_hlo_Strpyog_1_1
647	int_1_1
648	int315.5_1_1
649	murEStrpyog_1_1
650	oppA_1_1
651	oppCStrpyog_1_1
652	oppD_1_1
653	SPy0382Strpyog_1_1
654	SPy0390Strpyog_1_1

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<i>Streptococcus pyogenes</i> identification	
655	SpyM3_1351_1_1
656	vicXStrpyog_1_1
<i>Streptococcus viridans</i> identification	
687	573Stprmut_1_1
688	580SStprmut_1_1
689	581_582SStprmut_1_1
690	584SStprmut_1_1
691	dltAStrmut_1_1
692	dltBStrmut_1_1
693	dltCppx1Strmut_1_1
694	dltDStrmut_1_1
695	lichStrbov_1_1
696	lytRStprmut_1_1
697	lytSStprmut_1_1
698	pepQStrmut_1_1
699	pflCStrmut_1_1
700	recNStprmut_1_1
701	ytqBStrmut_1_1
<i>Proteus mirabilis</i> identification	
706	atfA_1_1
707	atfB_1_1
708	atfC_1_1
709	ccmPrmi1_1_1
710	cyaPrmi_1_1
711	aad_1_1
712	flfB_1_1
713	flfD_1_1
714	flfN_1_1
715	flhD_1_1
716	floA_1_1
717	ftsK_1_1
718	gstB_1_1
719	hemCPrmi_1_1
720	hemDPrmi_1_1
721	hev_1_1
722	katA_1_1
723	lpp1_1_1
724	menE_1_1

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(continued)

<i>Proteus mirabilis</i> identification	
725	mfd_1_1
726	nrpA_1_1
727	nrpB_1_1
728	nrpG_1_1
729	nrpS_1_1
730	nrpT_1_1
731	nrpU_1_1
732	pat_1_1
733	pmfA_1_1
734	pmfC_1_1
735	pmfE_1_1
736	ppaA_1_1
737	rsbA_1_1
738	rsbC_1_1
739	speB_1_1
740	stmA_1_1
741	stmB_1_1
742	terA_1_1
743	terD_1_1
744	umoA_1_1
745	umoB_1_1
746	umoC_1_1
747	ureR_1_1
748	xerC_1_1
749	ygbA_1_1
<i>Proteus vulgaris</i> identification	
776	envZPrvu_1_1
777	frdC_1_1
778	frdD_1_1
779	infBPrvu_1_1
780	lad_1_1
781	tna2_1_1

b) virulence gene probes

SEQ ID NO	Probe
<i>Staphylococcus aureus</i> virulence	
100	bsaE_1_1
101	bsaG_1_1

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(continued)

SEQ ID NO	Probe
<i>Staphylococcus aureus</i> virulence	
102	cap5h_1_1
103	cap5i_1_1
104	cap5j_1_1
105	cap5k_1_1
106	cap8H_1_1
107	cap8I_1_1
108	cap8J_1_1
109	cap8K_1_1
110	l-hld_1_1
111	l-hysA_1_1
112	l-IgGbg_1_1
113	EDIN_1_1
114	eta_1_1
115	etb_1_1
116	hglA_1_1
117	hglA_2_1
118	hglB_1_1
119	hglC_2_1
120	hla_1_1
121	hlb_1_2
122	lukF_1_1
123	lukS_1_1
124	lukS_2_1
125	NAG_1_1
126	sak_1_1
127	sea_1_1
128	seb_1_1
129	sec1_1_1
130	seg_1_1
131	seh_1_1
132	sel_1_1
133	set15_1_1
134	set6_1_1
135	set7_1_1
136	set8_1_1
137	sprV8_1_1
138	tst_1_1

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SEQ ID NO	Probe
<i>Staphylococcus aureus</i> virulence	
139	l-sdrC_1_1
140	l-sdrD_1_1
141	l-sdrE_1_1
<i>Escherichia coli</i> virulence	
153	b1202_1_1
154	eae_1_1
155	eltB_1_1
156	escR_1_1
157	escT_1_1
158	escU_1_1
159	espB_1_1
160	fes_1_1
161	fes_2_1
162	fteA_1_1
163	hlyA_1_1
164	hlyB_1_1
165	iucA_1_1
166	iucB_1_1
167	iucC_1_1
168	papG_1_1
169	rfbE_1_1
170	shuA_1_1
171	SLTII_1_1
172	toxA-LTPA_1_1
173	VT2vaB_1_1
<i>Staphylococcus epidermidis</i> virulence	
200	gcaD_1_1
201	hld_orf5_1_1
202	icaC_1_1
203	icaD_1_1
204	icaR_1_1
205	psm_beta1and2_1_1
206	purR_1_1
207	spoVG_1_1
208	yabJ_1_1
<i>Staphylococcus haemolyticus</i> virulence	
215	lipShaem olyt_1_1

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<i>Staphylococcus lugdunensis</i> virulence	
220	slushABCStalugd_1_1
221	fblStalugd_1_1
<i>Staphylococcus warneri</i> virulence	
230	gehASTwar_1_1
<i>Candida albicans</i> virulence	
292	CCN1_1_1
293	CDC28_1_1
294	CLN2_1_1
295	CPH1_1_1
296	CYB1_1_1
297	EFG1_1_1
298	MNT1_1_1
299	RBF1_1_1
300	RBF1_2_1
301	RIM101_1_1
302	RIM8_1_1
303	SEC14_1_1
304	SEC4_1_1
305	TUP1_1_1
306	YPT1_1_1
307	ZNF1CZF1_2_1
<i>Enterococcus faecalis</i> virulence	
343	asa1_1_1
344	asp1_1_1
345	cgh_1_1
346	cylA_1_1
347	cylB_1_1
348	cylI_1_1
349	cylL_cylS_1_1
350	cylM_1_1
351	ace_1_1
352	ef00108_1_1
353	ef00109_1_1
354	ef0011_1_1
355	ef00113_1_1
356	ef0012_1_1
357	ef0022_1_1
358	ef0031_1_1

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<i>Enterococcus faecalis</i> virulence	
359	ef0032_1_1
360	ef0040_1_1
361	ef0058_1_1
362	enlA_1_1
363	esa_1_1
364	esp_1_1
365	gelE_1_1
366	groEL_1_1
367	groES_1_1
368	rt1_1_1
369	sala_1_1
370	salb_1_1
371	sea1_1_1
372	sep1_1_1
373	vicK_1_1
374	yycH_1_1
375	yycI_1_1
376	yycJ_1_1
<i>Enterococcus faecium</i> virulence	
394	entA_entl_1_1
395	entD_1_1
396	entR_1_1
397	oep_1_1
398	sagA_1_2
<i>Klebsiella pneumoniae</i> virulence	
432	cim_1_1
433	aldA_1_1
434	aldA_2_1
435	hemly_1_1
436	pSL017_1_1
437	pSL020_1_1
438	rcaA_1_1
439	rmlC_1_1
440	rmlD_1_1
441	waaG_1_1
442	wbbD_1_1
443	wbbM_1_1
444	wbbN_1_1

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<i>Klebsiella pneumoniae</i> virulence	
445	wbdA_1_1
446	wbdC_1_1
447	wztKpn_1_1
448	yibD_1_1
<i>Pseudomonas aeruginosa</i> virulence	
491	aprA_1_1
492	aprE_1_1
493	ctx_1_2
494	algB_1_1
495	algN_1_1
496	algR_1_1
497	ExoS_1_1
498	fvpA_1_1
499	lasRa_1_1
500	lipA_1_1
501	lipH_1_1
502	Orf159_1_2
503	Orf252_1_1
504	pchG_1_1
505	PhzA_1_1
506	PhzB_1_1
507	PLC_1_1
508	plcN_1_1
509	plcR_1_1
510	pvdD_1_1
511	pvdF_1_2
512	pyocinS1_1_1
513	pyocinS1im_1_1
514	pyocinS2_1_1
515	pys2_1_1
516	pys2_2_1
517	rbf303_1_1
518	rhIA_1_1
519	rhIB_1_1
520	rhIR_1_1
521	TnAP41_1_2
522	toxA_1_1

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<i>Streptococcus pneumoniae</i> virulence	
592	igaStrpneu_1_1
593	lytA_1_1
594	nanA_1_1
595	nanBStrpneu_1_1
596	pcpCStrpneu_1_1
597	ply_1_1
598	prtAStrpneu_1_1
599	pspA_1_2
600	SP0834Strpneu_1_1
601	SP0834Strpneu_1_2
602	sphtraStrpneu_1_1
603	wciJStrpneu_1_1
604	wziyStrpneu_1_1
605	wzxStrpneu_1_1
<i>Streptococcus agalactiae</i> virulence	
640	CAMPfactor_1_1
641	CAMPfactor_2_1
642	0499Straqa_1_1
643	hylStragal_1_1
644	lipStragal_1_1
<i>Streptococcus pyogenes</i> virulence	
657	DNaseIStrpyog_1_1
658	fba2Strpyog_1_1
659	fhuAStrpyog_1_1
660	fhuB1Strpyog_1_1
661	fhuDStrpyog_1_1
662	fhuGStrpyog_1_1
663	hylA_1_1
664	hylP_1_1
665	hyIP2_1_1
666	oppB_1_1
667	ropB_1_1
668	scpAStrpyog_1_1
669	sloStrpyog_1_1
670	smez-4Strpyog_1_1
671	sof_1_1
672	sof_2_1
673	speA_1_1

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<i>Streptococcus pyogenes</i> virulence	
674	speB2Strpyog_1_1
675	speCStrpyog_1_1
676	speJStrpyog_1_1
677	srtBStrpyog_1_1
678	srtCStrpyog_1_1
679	srtEStrpyog_1_1
680	srtFStrpyog_1_1
681	srtGStrpyog_1_1
682	srtIStrpyog_1_1
683	srtKStrpyog_1_1
684	srtRStrpyog_1_1
685	srtTStrpyog_1_1
686	vicKStrpyog_1_1
<i>Streptococcus viridans</i> virulence	
702	hlyXStrmut_1_1
703	igaStrmitis_1_1
704	igaStrsanguis_1_1
705	perMStrmut_1_1
<i>Proteus mirabilis</i> virulence	
750	flaA_1_1
751	flaD_1_1
752	fliA_1_1
753	hpmA_1_1
754	hpmB_1_1
755	lpsPrmi_1_1
756	mrpA_1_1
757	mrpB_1_1
758	mrpC_1_1
759	mrpD_1_1
760	mrpE_1_1
761	mrpF_1_1
762	mrpG_1_1
763	mrpH_1_1
764	mrpI_1_1
765	mrpJ_1_1
766	patA_1_1
767	putA_1_1
768	uca_1_1

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<i>Proteus mirabilis</i> virulence	
769	ureDP _{Prmi_1_1}
770	ureEP _{Prmi_1_1}
771	ureFP _{Prmi_1_1}
772	zapA_1_1
773	zapB_1_1
774	zapD_1_1
775	zapE_1_1
<i>Proteus vulgaris</i> virulence	
782	end_1_1
783	pqrA_1_1
784	urg_1_1

c) resistance gene probes

SEQ ID NO	Probe
Beta-lactams resistance	
785	blaIMP-7_1_1
786	mecISepid_1_1
787	blaOXA-10_1_2
788	blaB_1_1
789	ampC_1_1
790	I-blaR_1_1
791	blaOXA-32_1_1
792	bla-CTX-M-22_1_1
793	pbp2aStrpneu_1_1
794	blaSHV-1_1_1
795	blaOXA-2_1_1
796	blaRShaemolyt_1_1
797	blaIMP-7_1_2
798	I-mecR_1_1
799	blaOXY_1_1
800	dacCStrpyog_1_1
801	femA_1_1
802	mecA_1_1
803	blaShaemolyt_1_1
804	blavim_1_1
805	pbp2b_1_1
806	pbp2primeSepid_1_1
807	pbp2x_1_1

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SEQ ID NO	Probe
Beta-lactams resistance	
808	pbp3Saureuc_1_1
809	pbp4_1_1
810	pbp5Efaecium_1_1
811	pbpC_1_1
812	l-mecI_1_1
813	pbp1a_1_1
814	l-blal_1_1
815	blaTEM-106_1_1
816	blaOXY-KLOX_1_1
817	ftsWEF_1_1
818	fmhB_1_1
819	cumA_1_1
820	fem BShaem olyt_1_1
821	blaPER-1_1_1
822	bla_FOX-3_1_1
823	blaA_1_1
824	psrb_1_1
825	fmhA_1_1
826	mecRiSepid_1_1
827	blaZ_1_1
828	blaOXA-1_1_1
829	fox-6_1_1
830	blaPrmi_1_1
Aminoglycosides resistance	
831	aacA_aphDStwar_1_1
832	aacC1_1_2
833	aacC2_1_1
834	strB_1_1
835	aadA_1_1
836	aadB_1_2
837	aadD_1_1
838	aacA4_1_2
839	strA_1_1
840	aph-A3_1_1
841	aacC1_1_1
842	aacA4_1_1
843	aacA-aphD_1_1

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Aminoglycosides resistance	
844	l-spc_1_1
845	aphA3_1_1
Macrolide-Lincosamide-Streptogramin resistance	
846	ermC_1_1
847	linB_1_1
848	satSA_1_1
849	mdrSA_1_1
850	l-linA_1_1
851	ermB_1_2
852	ermA_1_1
853	satA_1_1
854	msrA_1_1
855	mphBM_1_1
856	mefA_1_1
857	mrX_1_1
Trimethoprim resistance	
858	dfrStrpneu_1_1
859	dfrA_1_1
Chloramphenicol resistance	
860	cmlA5_1_1
861	catEfaecium_1_1
862	cat_1_1
Tetracyclines resistance	
863	tetAJ_1_1
864	tetL_1_1
865	tetM_1_1
Glycopeptides resistance	
866	vanH(tn)_1_1
867	vanA_1_1
868	vanHB2_1_1
869	vanR_1_1
870	vanRB2_1_1
871	vanS(tn)_1_1
872	vanSB2_1_1
873	vanWB2_1_1
874	ddl_1_1
875	ble_1_1
876	vanXB2_1_1

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Glycopeptides resistance	
877	vanY(tn)_1_1
878	vanYB2_1_1
879	vanB_1_1
880	vanZ(tn)_1_1
881	vanC-2_1_1
882	vanX(tn)_1_1
Other / multiple substances resistance	
883	acrB_1_1
884	mexB_1_2
885	I-qacA_1_1
886	sull_1_1
887	sul_1_1
888	cadBStalugd_1_1
889	mexA_1_1
890	acrR_1_1
891	emeA_1_1
892	acrA_1_1
893	rtn_1_1
894	abcXStrpmut_1_1
895	qacEdelta1_1_1
896	elkT-abcA_1_1
897	I-cadA_1_1
898	albA_1_1
899	wzm_1_1
900	msrCb_1_1
901	nov_1_1
902	wzt_1_1
903	wbbI_1_1
904	norA23_1_1
905	mexR_1_1
906	arr2_1_1
907	mreA_1_1
908	I-cadC_1_1
909	uvrA_1_1
<i>Candida albicans</i> drug resistance	
910	CRD2_1_1
911	CDR1_1_1

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<i>Candida albicans</i> drug resistance	
912	CDR1_2_1
913	MET3_1_1
914	FET3_1_1
915	FTR2_1_1
916	MDR1-7_1_1
917	ERG11_1_1
918	SEC20_1_1

d) controls and utility genes

SEQ ID NO	Probe
Negative Controls	
919	rbcl_1_1
925	rbcl_1_1 1_2
Positive controls / human genes	
920	LDHA(hu)_1_1
921	GAPD(hu)_1_1
922	b-Act(hu)_1_1
923	ARHGDIA(hu)_1_1
924	PGK1 (hu)_1_1
Positive controls / 16S	
926	16SPa_1_1
927	23SEfaecium_2_1
928	16SStrepypog_1_1
929	16SStrepneu_1_1
930	16SStrepagalactiae_1_1
931	16SEfaecium_1_1
932	16SEfaecium_2_1
933	16SRNAEf_2_1
934	16SKpn_1_1
935	16SSa_3_1
936	16SRNAEf_1_1
937	16SShominis_1_1
938	16SShaemolyt_1_1
939	23SEfaecium_1_1
940	16SrRNAPrmi_1_1
941	16SrRNAPrvu1_1_1

(continued)

Positive controls / 16S	
942	16SSa_1_1
943	16SKlox_1_1
Positive controls / Spiked Controls	
944	p53_1_1
945	0135mihck_1_1
946	FAN_1_1
947	0270cap_1_1

[0059] The DNA microarray of (1) is preferably suitable for

(I) identification of *Staphylococcus aureus* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:1-99, preferably at least the gene probes represented by SEQ ID NO:71 and 68; and/or

(II) identification of *Escherichia coli* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:142-152, preferably at least the gene probes represented by SEQ ID NO: 143 and 149; and/or

(III) identification of *Staphylococcus epidermidis* and comprises gene probes of group (a) selected from SEQ ID NO:174-199, preferably at least the gene probes represented by SEQ ID NO: 177 and 184; and/or

(IV) identification of *Staphylococcus haemolyticus* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:209-214, preferably at least the gene probes represented by SEQ ID NO:209 and 210; and/or

(V) identification of *Staphylococcus lugdunensis* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:216-219, preferably at least the gene probes represented by SEQ ID NO:216 and 219; and/or

(VI) identification of *Staphylococcus warneri* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:224-229, preferably at least the gene probes represented by SEQ ID NO:224 and 225; and/or

(VII) identification of *Candida albicans* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:231-291, preferably at least the gene probes represented by SEQ ID NO:231 and 232; and/or

(VIII) identification of *Enterococcus faecalis* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:308-342, preferably at least the gene probes represented by SEQ ID NO:308 and 310; and/or

(IX) identification of *Enterococcus faecium* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:377-393, preferably at least the gene probes represented by SEQ ID NO:377 and 380; and/or

(X) identification of *Klebsiella pneumonia* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:399-431, preferably at least the gene probes represented by SEQ ID NO:399 and 402; and/or

(XI) identification of *Klebsiella oxytoca* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:449-469, preferably at least the gene probes represented by SEQ ID NO:449 and 455; and/or

(XII) identification of *Pseudomonas aeruginosa* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:470-490, preferably at least the gene probes represented by SEQ ID NO:470 and 471 ; and/or

(XIII) identification of *Streptococcus pneumoniae* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:523-591, preferably at least the gene probes represented by SEQ ID NO:523 and 524; and/or

(XIV) identification of *Streptococcus agalactiae* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:606-639, preferably at least the gene probes represented by SEQ ID NO:606 and 619; and/or

(XV) identification of *Streptococcus pyogenes* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:645-656, preferably at least the gene probes represented by SEQ ID NO:645 and 646; and/or

(XVI) identification of *Streptococcus viridans* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:687-701, preferably at least the gene probes represented by SEQ ID NO:687 and 691 ; and/or

(XVII) identification of *Proteus mirabilis* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:706-749, preferably at least the gene probes represented by SEQ ID NO:706 and 710; and/or

(XVIII) identification of *Proteus vulgaris* and comprises one or more or all gene probes of group (a) selected from SEQ ID NO:776-781, preferably at least the gene probes represented by SEQ ID NO:776 and 777.

[0060] In a further especially preferred aspect, the DNA microarray of (1) is suitable for

(I) virulence determination of *Staphylococcus aureus* and comprises one or more or all of the gene probes of group

(b) selected from SEQ ID NO:100-141 ; and/or
 (II) virulence determination of *Escherichia coli* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO: 153-173; and/or
 (III) virulence determination of *Staphylococcus epidermidis* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:200-208; and/or
 (IV) virulence determination of *Staphylococcus haemolyticus* and comprises the gene probe of group (b) represented by SEQ ID NO:215; and/or
 (V) virulence determination of *Staphylococcus lugdunensis* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:220-221 ; and/or
 (VI) virulence determination of *Staphylococcus warneri* and comprises the gene probe of group (b) represented by SEQ ID NO:230; and/or
 (VII) virulence determination of *Candida albicans* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:292-307; and/or
 (VIII) virulence determination of *Enterococcus faecalis* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:343-376; and/or
 (IX) virulence determination of *Enterococcus faecium* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:394-398; and/or
 (X) virulence determination of *Klebsiella pneumonia* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:432-448; and/or
 (XI) virulence determination of *Klebsiella oxytoca*; and/or
 (XII) virulence determination of *Pseudomonas aeruginosa* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:491-522; and/or
 (XIII) virulence determination of *Streptococcus pneumoniae* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:592-605; and/or
 (XIV) virulence determination of *Streptococcus agalactiae* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:640-644; and/or
 (XV) virulence determination of *Streptococcus pyogenes* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:657-686; and/or
 (XVI) virulence determination of *Streptococcus viridans* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:702-705; and/or
 (XVII) virulence determination of *Proteus mirabilis* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO:750-775; and/or
 (XVIII) virulence determination of *Proteus vulgaris* and comprises one or more or all of the gene probes of group (b) selected from SEQ ID NO: 782-784.

[0061] In a further especially preferred aspect, the DNA microarray of (1) is suitable for antibiotic resistance determination of (I) *Staphylococcus aureus*, (II) *Escherichia coli*, (III) *Staphylococcus epidermidis*, (IV) *Staphylococcus haemolyticus*, (V) *Staphylococcus lugdunensis*, (VI) *Staphylococcus warneri*, (VIII) *Enterococcus faecalis*, (IX) *Enterococcus faecium*, (X) *Klebsiella pneumonia*, (XI) *Klebsiella oxytoca*, (XII) *Pseudomonas aeruginosa*, (XIII) *Streptococcus pneumoniae*, (XIV) *Streptococcus agalactiae*, (XV) *Streptococcus pyogenes*, (XVI) *Streptococcus viridans*, (XVII) *Proteus mirabilis*, and/or (XVIII) *Proteus vulgaris* and comprises one or more or all of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

[0062] it is suitable for antibiotic resistance determination of (VII) *Candida albicans* and comprises one or more or all of the gene probes of group (c) selected from SEQ ID NO:910-918.

[0063] In a preferred embodiment, the microarray of (1) is suitable for identification and characterisation, i.e. virulence and/or resistance determination, of the target microorganism and comprises one or more or all of the gene probes of group (a) and additionally one or more or all of the gene probes of group (b) and group (c) for each organism as listed above

[0064] If the identification and/or characterisation of *S. aureus*, *E. coli* and/or *P. aeruginosa* is the aim of a test using the array, then the array comprises preferably at least the core gene probes designated in example 7, more preferably all the sequences listed in Tab. 2 and/or Tab. 6. Even more preferred, it consists of said sequences.

[0065] In a most especially preferred aspect, the DNA microarray of (1) comprises the following gene probes, even more preferably consists of the following gene probes:

(I) When the DNA microarray is suitable for identification and characterisation of *Staphylococcus aureus*, it comprises

- (a) the gene probes represented by SEQ ID NO: 1-99; and
- (b) the gene probes represented by SEQ ID NO:100-141 and/or
- (c) the gene probes represented by SEQ ID NO:785-909.

(II) When the DNA microarray is suitable for identification and characterisation of *Escherichia coli*, it comprises

- (a) the gene probes represented by SEQ ID NO: 142-152; and
- (b) the gene probes represented by SEQ ID NO: 153-173 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(III) When the DNA microarray is suitable for identification and characterisation of *Staphylococcus epidermidis*, it comprises

- (a) the gene probes represented by SEQ ID NO: 174-199; and
- (b) the gene probes represented by SEQ ID NO: 200-208 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(IV) When the DNA microarray is suitable for identification and characterisation of *Staphylococcus haemolyticus*, it comprises

- (a) the gene probes represented by SEQ ID NO: 209-214; and
- (b) the gene probes represented by SEQ ID NO: 215 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(V) When the DNA microarray is suitable for identification and characterisation of *Staphylococcus lugdunensis*, it comprises

- (a) the gene probes represented by SEQ ID NO: 216-219; and
- (b) the gene probes represented by SEQ ID NO: 220-221 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(VI) When the DNA microarray is suitable for identification and characterisation of *Staphylococcus warneri*, it comprises

- (a) the gene probes represented by SEQ ID NO: 224-229; and
- (b) the gene probes represented by SEQ ID NO: 230 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(VII) When the DNA microarray is suitable for identification and characterisation of *Candida albicans*, it comprises

- (a) the gene probes represented by SEQ ID NO: 231 -291 ; and
- (b) the gene probes represented by SEQ ID NO: 292-307 and/or
- (c) the gene probes represented by SEQ ID NO: 910-918.

(VIII) When the DNA microarray is suitable for identification and characterisation of *Enterococcus faecalis*, it comprises

- (a) the gene probes represented by SEQ ID NO: 308-342; and
- (b) the gene probes represented by SEQ ID NO: 343-376 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(IX) When the DNA microarray is suitable for identification and characterisation of *Enterococcus faecium*, it comprises

- (a) the gene probes represented by SEQ ID NO: 377-393; and
- (b) the gene probes represented by SEQ ID NO: 394-398 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(X) When the DNA microarray is suitable for identification and characterisation of *Klebsiella pneumonia*, it comprises

- (a) the gene probes represented by SEQ ID NO: 399-431; and
- (b) the gene probes represented by SEQ ID NO: 432-448 and/or
- (c) the gene probes represented by SEQ ID NO: 785-909.

(XI) When the DNA microarray is suitable for identification and characterisation of *Klebsiella oxytoca*, it comprises

- (a) the gene probes represented by SEQ I D NO: 449-469, and
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XII) When the DNA microarray is suitable for identification and characterisation of *Pseudomonas aeruginosa*, it comprises

- (a) the gene probes represented by SEQ I D NO: 470-490; and
- (b) the gene probes represented by SEQ I D NO: 491 -522 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XIII) When the DNA microarray is suitable for identification and characterisation of *Streptococcus pneumoniae*, it comprises

- (a) the gene probes represented by SEQ I D NO: 523-591 ; and
- (b) the gene probes represented by SEQ I D NO: 592-605 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XIV) When the DNA microarray is suitable for identification and characterisation of *Streptococcus agalactiae*, it comprises

- (a) the gene probes represented by SEQ I D NO: 606-639; and
- (b) the gene probes represented by SEQ I D NO: 640-644 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XV) When the DNA microarray is suitable for identification and characterisation of *Streptococcus pyogenes*, it comprises

- (a) the gene probes represented by SEQ I D NO: 645-656; and
- (b) the gene probes represented by SEQ ID NO: 657-686 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XVI) When the DNA microarray is suitable for identification and characterisation of *Streptococcus viridans*, it comprises

- (a) the gene probes represented by SEQ I D NO: 687-701 ; and
- (b) the gene probes represented by SEQ I D NO: 702-705 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XVII) When the DNA microarray is suitable for identification and characterisation of *Proteus mirabilis*, it comprises

- (a) the gene probes represented by SEQ I D NO: 706-749; and
- (b) the gene probes represented by SEQ I D NO: 750-775 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

(XVIII) When the DNA microarray is suitable for identification and characterisation of *Proteus vulgaris*, it comprises

- (a) the gene probes represented by SEQ I D NO: 776-781 ; and
- (b) the gene probes represented by SEQ I D NO: 782-784 and/or
- (c) the gene probes represented by SEQ I D NO: 785-909.

[0066] The microarray of embodiment (1) can be fabricated using textbook methods for microarray production, including printing with fine-pointed pins onto the solid support, photolithography using pre-made masks or dynamic micromirror devices, ink-jet printing or electrochemistry on microelectrode arrays (Müller, H.-J., Röder, T., "Der Experimentator: Microarrays, Spektrum Akademischer Verlag, Heidelberg (2004)). Preferred fabrication methods are printing methods spotting the gene probes onto the solid surface of the microarray. The attachment of the spotted DNA to the surface is achieved by covalent or non-covalent binding, preferably by non-covalent binding, more preferably by electrostatic

interaction (ionic binding), most preferably by ionic binding of the DNA to amino groups present on the surface of the solid support. Any amino-functionalized microarray support can be used, but gamma aminopropyl silane (GAPS™) coated slides, especially UltraGAPS™ coated glass slides, are preferred in present invention.

[0067] The amount of DNA per spot printed onto the array is from 0.1 to 15.0 ng, preferably from 0.1 to 0.2 ng.

[0068] Thus, the present invention also pertains to a method for fabrication of a microarray of embodiment (1), which method comprises spotting the gene probes listed above to an appropriate solid support.

[0069] The sample or clinical specimen of embodiment (1) is preferably selected from the group consisting of whole blood, serum, urine, saliva, liquor, sputum, punktate, stool, pus, wound fluid and positive blood cultures, more preferably is whole blood or a positive blood culture, most preferably is a positive blood culture. If blood culture is used as DNA source, 0.5 ml positive blood culture is sufficient for identification and characterisation of the microorganisms and bacteria present without prior amplification of the target DNA.

[0070] Thus, the microarray of present application is

- (i) a robust diagnostic tool, detecting all tested bacterial reference strains and clinical isolates;
- (ii) sensitive enough to yield positive signals with e.g. only 20 ng of purified genomic *S. aureus* DNA or 2 µg of DNA extracted from blood culture which contains a high percentage of human DNA;
- (iii) highly specific, distinguishing e.g. *S. aureus* from distantly related gram-negative bacteria like *Escherichia coli* or *Pseudomonas aeruginosa* as well as from closely related CoNS;
- (iv) precise enough to identify virulence factors and antibiotic resistance determinant genes without previous amplification by PCR.

[0071] Moreover, the whole procedure can be accomplished the same day after blood cultures become positive (e.g. in the Bactec®). Rapid identification of the causative pathogen in fungemia, bacteremia and sepsis is crucial for several reasons:

- (i) appropriate antimicrobial therapy should be started as early as possible and unnecessary treatment avoided;
- (ii) the prognosis of the patients with sepsis may be improved; and
- (iii) expenditures on antimicrobials and prolonged hospitalisation can be reduced.

[0072] With the gene-segment based microarray of (1) there is an excellent correlation between genotypic detection of antibiotic resistance determinants and phenotypic typing using conventional susceptibility testing. In one aspect of the invention, the detection of the resistance genes *mecA*, *blaZ*, *ermA*, *ermC*, *msrSA*, *aadD* and *aacA-aphD* by microarray hybridisation allows for reliable prediction of oxacillin, penicillin, erythromycin, tobramycin and gentamicin resistance in a single assay.

[0073] By microarray hybridisation according to present invention it is furthermore possible to discriminate multi-resistant and multi-susceptible MRSA (strain MW2). Multi-susceptible MRSA have been shown to be susceptible to tobramycin and erythromycin (Polyzou, A. et al., J. Antimicrob. Chemother. 48:231-4 (2001); Pournaras, S. et al., J. Clin. Microbiol. 39:779-81 (2001)).

[0074] In a preferred aspect of the invention, simultaneous comprehensive resistance genotyping for oxacillin, macrolide and aminoglycoside resistance genes (preferably *mecA*, *aadD*, *aacA-aphD*, *ermA,B,C* and *msrSA*) by microarray hybridisation allows the rapid discrimination of multi-resistant or multi-susceptible strains and in consequence other therapeutic options with e.g. macrolides and may reduce reliance on vancomycin (Polyzou, A. et al., J. Antimicrob. Chemother. 48:231-4 (2001); Pournaras, S. et al., J. Clin. Microbiol. 39:779-81 (2001)).

[0075] One preferred aspect of embodiment (1) is a DNA microarray for the identification and characterisation of the three important bacteremia causing species *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* in a sample, preferably in blood culture. The microarray allows simultaneous species identification and detection of important virulence and antibiotic resistance genes in a single assay. Preferably, this array consists of 2-20 species specific gene probes, 1-20 virulence gene probes and 1-20 resistance gene probes of at least 100 nt length, more preferably of 200-800 nt length. One especially preferred embodiment is an array comprising or consisting of the gene probes listed in Tab. 2. The probes may be amplified from recombinant plasmids or synthesized by any other method known in the art. These probes represent genes encoding house-keeping proteins, virulence factors and antibiotic resistance determinants. Evaluation with 42 clinical isolates, 3 reference strains and 13 positive blood cultures revealed that this DNA microarray is highly specific in identifying *S. aureus*, *E. coli* and *P. aeruginosa* strains and in discriminating them from closely related Gram-positive and Gram-negative bacterial strains also known to be etiological agents of bacteremia. In Example 6 and 7, this array was successful in identifying all tested 27 *E. coli*, *P. aeruginosa* and *S. aureus* strains and in discriminating them from 21 closely related Gram positive and Gram negative bacterial strains. There is a nearly perfect correlation between genotypic antibiotic resistance by hybridisation to the *S. aureus* resistance gene probes *mecA* (oxacillin/methicillin resistance), *aacA-aphD* (gentamicin resistance), *ermA* (erythromycin resistance)

and *blaZ* (penicillin resistance) and the *E. coli* resistance gene probes *blaTEM-106* (penicillin resistance) and *aacC2* (aminoglycoside resistance) and phenotypic antibiotic resistance determined by conventional susceptibility testing (Example 10).

[0076] One further preferred aspect of embodiment (1) of the invention is a DNA microarray for the identification and characterisation of *S. aureus* in a sample, preferably in blood culture. Evaluation with 10 clinical isolates, 6 reference strains and 10 positive blood cultures revealed that this DNA microarray is highly specific in identifying *S. aureus* and in discriminating them from closely related Gram-positive and Gram-negative bacterial strains also known to be etiological agents of bacteremia (Example 11).

[0077] The method of embodiment (3) comprises - after isolating the total DNA (including non-microbial DNA) from a sample - the steps of immediate labelling and microarray-based detection of this isolated DNA with or without, preferably without, further DNA amplification steps after the DNA isolation. It is one advantage of the method (3) that it can be performed without said further DNA amplification steps, i.e. the isolated DNA is labelled and applied to the microarray without prior amplification. The use of a single protocol for all microbial species comprising all steps of a microarray procedure including DNA preparation and DNA-chip hybridisation, is essential for testing blood cultures or other clinical specimens, where the bacterial diagnosis is usually uncertain. Preferably, a DNA preparation protocol employing sonication for simultaneous cell disruption and target DNA fragmentation is the method of choice to increase the sensitivity of the microarray, in particular towards low-copy number and/or plasmid encoded genes which may be underrepresented in the target DNA.

[0078] The method of embodiment (3) is preferably a method for diagnosis of bacteremia or sepsis. Furthermore, the sample or clinical specimen used in embodiment (3) is preferably blood or derived from blood, more preferably is a blood culture. Most preferably, the clinical specimen is a positive blood culture.

[0079] To obtain positive signals in the method of embodiment (3), 100 pg of purified genomic microbial DNA may be sufficient (lower detection limit), but preferably at least 1 ng of said DNA should be present in the sample. Usually, at least 10 ng, preferably at least 20 ng, more preferably at least 1 µg of purified genomic microbial DNA or at least 1 µg, preferably at least 2 µg of DNA extracted from blood culture are required. 500 µl of positive blood culture yield enough DNA for several hybridisations.

[0080] In the method of embodiment (3), the ratio of microbial DNA to total DNA isolated from said sample or clinical specimen is less than or equal to 100 %, preferably is from 1% to 99%, more preferably from 30 to 60%.

[0081] The labelling reaction of the method of embodiment (3) may be any DNA labelling reaction known in the art. However, chemical labelling reactions consisting of chemical attachment of a reporter molecule to the sample DNA and labelling by integration of labelled nucleotides into the sample DNA are preferred. Preferably the reporter molecules are fluorophores, more preferably are of the cyanine group of fluorophores. Most preferably, the DNA is labelled with Cy3, Cy5 and/or Alexa Fluor 647 and Alexa Fluor 546. The ratio of bases to dye molecules (BDR) is preferably less or equal to 60.

[0082] The detection of the reporter molecule in the method of embodiment (3) of the invention is preferably done by using a suitable detection system for the bound reporter molecule. This detection system is preferably based on visualization of the reporter molecule, more preferably on fluorescence detection. Furthermore, the detection is preferably done by a microarray scanner.

[0083] In the method of embodiment (3) of the invention, the DNA microarray can be substituted by any other solid support onto which DNA gene probes are attached in a way permitting hybridisation of the DNA in the sample and subsequent detection of the bound DNA. This includes the use of microtiter plates coated with one or several DNA gene probes per well, of glass surfaces (like, e.g., microscopic slides) with DNA spots, of filter paper disks, membranes, gold electrodes and beads (particles with a diameter of from 1 nm to several µm made of glass, plastic, metal etc.) coated with DNA, etc.

[0084] The kit of embodiment (4) of the invention may additionally comprise reagents for the labelling reactions of embodiment (3) and/or reagents necessary for the hybridisation step of the method of embodiment (3).

[0085] The present invention is described in more detail by reference to the following examples. It should be understood that these examples are for illustrative purpose only and are not to be construed as limiting the invention.

Examples

[0086] In the experimental examples described below, standard techniques of recombinant DNA technology were used that were described in various publications, e.g. Sambrook et al. (1989), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, or Ausubel et al. (1987), Current Protocols in Molecular Biology 1987-1988, Wiley Interscience. Unless otherwise indicated, all enzymes and kits were used according to the manufacturers' specifications.

Example 1 : Materials and Methods

[0087] Reference strains, clinical isolates and culture conditions: Bacterial reference strains were obtained from the American Type Culture Collection (ATCC, Manassas, Va.), the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ, Braunschweig, Germany) or the network on antimicrobial resistance in *Staphylococcus aureus* (NARSA, Herndon, Virginia). Clinical isolates were obtained from the inventors' clinical routine microbiology laboratory.

[0088] The following bacteria were used for evaluation of the specificity of the microarray in Examples 2-10: *Staphylococcus aureus* (ATCC 25923, NRS123 alias MW2, 5 clinical isolates), *Staphylococcus epidermidis* (5 clinical isolates), *Staphylococcus capitis* (clinical isolate), *Staphylococcus haemolyticus* (clinical isolate), *Staphylococcus hominis* (clinical isolate), *Staphylococcus warneri* (clinical isolate), *Staphylococcus auricularis* (clinical isolate), *Micrococcus* spp. (clinical isolate), *Escherichia coli* (ATCC 25922, 6 clinical isolates), *Pseudomonas aeruginosa* (ATCC27853, 5 clinical isolates), *Klebsiella pneumoniae* (3 clinical isolates), *Proteus mirabilis* (2 clinical isolates), *Serratia marcescens* (2 clinical isolates), *Enterobacter cloacae* (clinical isolate), *Enterobacter aerogenes* (clinical isolate), *Acinetobacter baumannii* (clinical isolate), *Stenotrophomonas maltophilia* (clinical isolate), *Enterococcus* spp. (clinical isolate), *Enterococcus faecalis* (clinical isolate) and *Streptococcus pneumoniae* (clinical isolate).

[0089] Bacterial strains and clinical isolates were grown over night at 37 °C with constant shaking in 5 ml Luria-Bertani (LB) broth or tryptic soy broth (TSB, 30 g/l, Merck) containing 3 g/l yeast extract. Enterococci and streptococci were grown in 10 ml TSB plus yeast without agitation under 5% CO₂. Overnight cultures were harvested at 2,560 g for 10 min. After discarding the supernatant the pellet was washed in 1 ml TE (10 mM Tris-HCl, pH 7.5 and 1 mM EDTA) and recovered by centrifugation at 17,900 g for 10 min. Cell pellets were used for DNA preparation.

[0090] Blood cultures: Aerobic and anaerobic blood culture bottles (BACTEC®, Becton Dickinson, Heidelberg, Germany) were inoculated with blood from patients with suspected sepsis and placed in a BACTEC® 9240 blood culture system (Becton Dickinson), a continuous-reading, automated, and computed blood culture system that detects the growth of microorganisms by monitoring CO₂ production. Incubation was performed according to the manufacturer's recommendations. Bottles with a positive growth index were removed from the incubator, and aliquots of 1 ml of the blood culture suspensions were taken aseptically with a needle syringe. 1 ml-aliquots of the blood culture suspensions were mixed with 1 ml 0.1% Triton®-X-100 and kept at room temperature for 5 min in order to disrupt human blood cells. Bacterial cells were then harvested at 17,900 g for 10 min, pellets were washed in 1 ml TE, recovered by centrifugation and used for DNA preparation. For conventional identification and susceptibility testing, a second 1 ml-aliquot was examined by Gram-stain and subcultured on agar plates. The organisms grown on agar plates were characterised and tested for susceptibility using a VITEK-2 system (bioMérieux, Inc., Nürtingen, Germany), Etest strips (AB BIODISK, Solna, Sweden) or disk diffusion tests following the method recommended by the National Committee for Clinical Laboratory Standards (NCCLS) (Standards, N.C.f.C.L., Approved standard M2-4a, Villanova, PA (1990)).

[0091] For microarray hybridisation experiments, DNA was prepared from 13 blood cultures positive for *S. aureus* (4), *S. epidermidis* (3), *S. pneumoniae* (2), *P. aeruginosa* (1), *E. coli* (2) and *P. mirabilis* (1).

Example 2: DNA preparation

[0092] Total cellular DNA was extracted and purified either by using the First-DNA All-tissue kit (GEN-IAL GmbH, Troisdorf, Germany) following the instructions of the supplier or by enzymatic lysis followed by phenol/chloroform extraction. For the latter protocol, cell pellets were resuspended in 500 µl lysis buffer (20 mM Tris-HCl, pH 8.0, 2 mM EDTA, pH 8.0, and 1.2% Triton®-X-100) and lysozyme (Sigma, Taufkirchen, Germany) was added to reach a final concentration of 0.8 mg/ml. In addition, lysostaphin (Sigma) was added to a final concentration of 0.2 mg/ml to promote staphylococcal lysis or mutanolysin (0.5 U/µl; Sigma) was added to lyse Streptococci and Enterococci. After incubation at 37°C for one hour, cell lysates were treated with Proteinase K (1 mg/ml; Sigma) for 1 hour at 55°C and then with RNase A (0.2 mg/ml; Qiagen, Hilden, Germany) for 1 hour at 37°C. The volume was increased by the addition of 200 µl TE and the salt concentration was adjusted to 0.7 M by addition of 5 M NaCl. A 10% CTAB (cetyltrimethylammonium bromide) solution in 0.7 M NaCl was added to a final concentration of 1% and incubated at 65°C for 20 min in order to release DNA from polysaccharide DNA complexes. DNA was then extracted once with phenol/chloroform/isoamyl alcohol (25:24:1) and once with chloroform/isoamyl alcohol (24:1) prior to precipitation with one volume of isopropanol. After centrifugation at 17,900 g for 30 min, DNA pellets were washed in 70% ethanol and resuspended in 50-100 µl TE.

[0093] Concentration, purity and size of the purified DNA preparations were determined by UV-spectrophotometry (lambda 40, PerkinElmer, Boston USA) and 1% agarose gel electrophoresis.

Example 3: DNA labelling

[0094] Total DNA from commercially available reference strains, clinical isolates and blood cultures was labelled by a non-enzymatic chemical labelling method using the Label It Cy3/Cy5 kits (Mirus, Madison, USA) or the ULYSIS Alexa

Fluor 467 Nucleic Acid Labelling Kit (Molecular Probes; Eugene, USA). Prior to labelling, each target DNA was spiked with three gene segments (1 µl each, 30 ng/µl) amplified by PCR from selected recombinant plasmids to serve as internal positive controls.

[0095] For labelling with the Label It Cy3/Cy5 kit 5 µg of high molecular weight DNA (>20 kb) were mixed with 7.5 µl reagent in a total volume of 50 µl and incubated for 2 hours at 37°C according to the recommendations by the supplier. After adjusting the volume to 200 µl with H₂O and adding 0.1 volume of 5 M NaCl, unbound label was removed by precipitation with 2 volumes of ice-cold absolute ethanol for at least 30 min at -20 °C. The labelled DNA was recovered by centrifugation at 17,900 g for 30 min. The pellet was washed with 70% ethanol and resuspended in 70 µl TE.

[0096] For labelling with the Ulysis Alexa Fluor 647 kit, 1 µg DNA was denatured at 95°C for 5 min, cooled on ice, mixed with 20 µl labelling buffer and 5 µl reagent and incubated at 80 °C for 15 min according to the instructions of the manufacturer. Unbound dye was removed by ethanol precipitation as described above. The relative labelling efficiency of a reaction was evaluated by calculating the approximate ratio of bases to dye molecules (acceptable labelling ratios for nucleic acid were =60). This ratio and the amount of recovered labelled DNA was determined by measuring the absorbance of the nucleic acids at 260 nm and the absorbance of the dye at its absorbance maximum using a lambda40 UV-spectrophotometer (PerkinElmer) and plastic disposable cuvettes for the range from 220 nm to 1,600 nm (UVette; Eppendorf, Hamburg, Germany).

Example 4: Microarray construction

[0097] Cloned PCR-products were used to generate probes for the DNA microarray. All together 120 gene segments representing virulence genes, antibiotic resistant determinants and species specific metabolic and structural genes from *S. aureus* (40), *E. coli* (31) and *P. aeruginosa* (49) were represented on the microarray (Tab. 2).

Tab. 2: Gene probes with SEQ ID NOs, function, gi numbers and primer sequences. *E. coli* gene probes (1-31), *P. aeruginosa* gene probes (32-80), *S. aureus* gene probes (81-120).

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
1	<i>envZ</i>	Inner membrane osmosensor	453286	143	AGCCTGGTGACGA CTTATC [1233]	ATCCGCCAGTTGCTT AAC [1234]
2	<i>fes(2)</i>	Enterochelin esterase (siderophore)	145916	161	TGTTTCTGCACTCG AAATG [1269]	GGCAATAGCTTTCAC CAG [1270]
3	<i>fes(1)</i>	Enterochelin esterase (siderophore)	145916	160	TGTTTGAGGTCAC TTCTGG [1267]	CAATAGCTTTCACCA GGG [1268]
4	<i>nfrB</i>	Bacteriophage N4 receptor, inner membrane protein	16127994	145	ATGGAATTGCGTCT GTTC [1237]	AAGTTTAGCCACAGC AGG [1238]
5	<i>yacH</i>	Putative membrane protein	16127994	148	GACTCGGTACAGC GATTG [1242]	CTGACGTTGGGTATC TCG [1243]
6	<i>yagX</i>	Putative enzyme	16127994	149	GTTTACGACGGTTC TCCC [1244]	AATCTCCCTGCTGA AATG [1245]
7	<i>ycdS</i>	Putative outer membrane protein	16127994	150	TTGAAACTTCTTAC TGCCG [1246]	AATTTCTAATGCAGC GTATTG [1247]
8	<i>b1169</i>		16127994	142	GTTTGGGACTTATT GCTCTG [1230]	CATCAGCCACAGTTT CAAG [1231]
9	<i>b1202</i>	Putative outer membrane protein	16127994	153	GAATACCAAAGCA GATCGTC [1252]	CCGAGATCGACAACA GAG [1253]
10	<i>fliCb</i>	Flagellar H antigen	8071787	144	ACCACGACAGGTC TTTATG [1234]	AGAGAGGCACCGTC ACTAC [1235]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
11	<i>iucA</i>	Aerobactin synthesis (siderophore)	474189	165	CATCAGGCAGTTAT CCTGTC [1276]	AGTCGTCCTCCTGCA TTAC [1277]
12	<i>iucB</i>	Aerobactin synthesis (siderophore)	474189	166	TTCACAGCGGATAT GGAC [1278]	CAC TTTGCTCCGAGA AATAC [1279]
13	<i>iucC</i>	Aerobactin synthesis (siderophore)	474189	167	AGACTGGGATTTG GTCAAC [1280]	AGACACCATCCTGCC TTC [1281]
14	<i>papG</i>	Adhesin, P-pil protein	42307	168	GGAGTATATTGCGT GGGTAG [1282]	AAGATTACCATAGAG GGCG [1283]
15	<i>yciQ</i>	Putative membrane protein	16127994	151	ATAGCAGGGCTGT TTGTATC [1248]	GACACGGAAACCAA ATTAAC [1249]
16	<i>ymcA</i>	Hypothetical protein	16127994	152	TATTGTCATCGCGC AGAG [1250]	TGTTGGTTGAAAAGA GTAGC [1251]
17	<i>eae</i>	Genetic locus necessary for the production of attaching and effacing lesions on tissue culture, OM protein adhesin	145852	154	CTAACTCATTTGTGG TGGAGC [1254]	CTTGTCATCGGTGAT GTTG [1255]
18	<i>eltB</i>	Enterotoxin subunit B	145830	155	GGCGTTACTATCCT CTCTATG [1256]	TTTCCATACTGATTG CCG [1257]
19	<i>escR</i>	Secretion	2897961	156	TTTGTGTTATTGG TACTTCATTC [1258]	ATCGAAATTGTTACT GGCG [1259]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
20	<i>escT</i>	Secretion	2897961	157	TTACGCTTCCGATC ATAGTAG [1260]	GAATACGTTTAGTTG AGGCG [1261]
21	<i>escU</i>	Secretion	2897961	158	AAGTGAAGAGGTA ATGGCTG [1262]	TACATCAGTATCCT TGGC [1263]
22	<i>espB</i>	Protein secreted by enteropathogenic E. coli	1657262	159	GATGGTGACTCTAT TGCAGG [1264]	CCATACGATTCTGGA CCTC [1265]
23	<i>hlyA</i>	Enterohemorrhagic Escherichia coli hemolysin	525328	163	CTTGAAATGTTGG TAAAGC [1272]	TAAATCCTTCGGTT GAGC [1273]
24	<i>hlyB</i>	Enterohemorrhagic Escherichia coli hemolysin	1247757	164	TCAATGCTGAAACT ATAAGGC [1274]	ACTTAGCACCCAGTT CGAC [1275]
25	<i>SLTII</i>	Shiga-like toxin type II	304950	171	TTCTTCGGTATCCT ATTCCC [1288]	TGTAGGTCCACTTC TTCC [1289]
26	<i>toxA-LTPA</i>	Subunit A of heat-labile enterotoxin	148027	172	AAATGGCGACAAAT TATACC [1290]	CTGGGTCTCCTCATT ACAAAG [1291]
27	<i>VT2va B</i>	Verotoxin-2 variant, beta- subunit, shiga-like toxin	148261	173	AAGAAGATGTTTAT GGCGG [1292]	GATTCACAGGTACTG GATTG [1293]
28	<i>aacC2</i>	aminoglycoside-(3)-N- acetyltransferase	45769	833	GACCGATCACCCCTA CGAG [2612]	CGAAATGCTTCTCAA GATAGG [2613]
29	<i>blaTE M-106</i>	Class A beta-lactamase	21464484	815	ACATCGAACTGGAT CTCAAC [2576]	TCTCAGCGATCTGTC TATTTC [2577]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
30	<i>strB</i>	Streptomycin resistance protein B	17129524	834	AAGTTTCATTGCCA GACG [2614]	TAGACTGCGTTGCTC CTC [2615]
31	<i>sul</i>	Dihydropteroate synthase, sulfonamide resistance	17129524	887	CATCGTCAACATAA CCTCG [2720]	AATTCTTGGGGTTTC TTTC [2721]
32	<i>algB</i>	Alginate biosynthesis (exopolysaccharide)	150990	494	CACTTTCCGTTATT GCCTC [1934]	GAGGATGAGGATGT TGGC [1935]
33	<i>algN</i>	Alginate biosynthesis (exopolysaccharide)	150999	495	GACTGGCTGAATC GTCTC [1936]	GCAGGTCGTACCAG GAAG [1937]
34	<i>algR</i>	Alginate biosynthesis (exopolysaccharide)	151003	496	ATTGTCGATGACGA ACCTC [1938]	TTCAGGTAGAGCTG GAAATG [1939]
35	<i>aprA</i>	Alkaline protease	45279	491	CATTGAAAGGTCGT AGCG [1928]	CGACGAAGTGGATA TTGG [1929]
36	<i>aprE</i>	Alkaline protease secretion	45279	492	GGTCAAGCACATC CTAGTG [1930]	ACTTCCTTGCGGTAC TCC [1931]
37	<i>glpR</i>	Repression of glycerol metabolic enzymes (glp-glycerol-3-phosphate)	1399486	470	CAAGCACAAACAAG AAATACG [1886]	TAGACCTCCGAAGA GTTGC [1887]
38	<i>lasR</i>	Elastase, virulence protein	309873	499	CTGGGACGTTAGT GTCATC [1944]	GTCTTGGCATTGAGT TCG [1945]
39	<i>lasR</i>	Transcriptional activator of elastase	151325	471	GAGCGACCTTGGA TTCTC [1888]	ATAAGACCCAAATTA ACGCG [1889]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward[SEQ ID NO]	Primer reverse [SEQ ID NO]
40	<i>lipA</i>	Extracellular triacylglycerol lipase	45340	500	AAGAAGTCTCTGCT CCCC [1946]	ACGATTTCTCTCCACC TGT [1947]
41	<i>lipH</i>	Lipophilic protein necessary for the expression of active lipase	483463	501	ATGGCAGTTTCAGT GTCG [1948]	CGAAATAGTCGTCCA GCC [1949]
42	<i>mexA</i>	Multidrug resistance protein MexA precursor	5616092	889	CTCGACCCGATCTA CGTC [2724]	GTCCTCACCTCGACA CCC [2725]
43	<i>Ori25 2</i>	DnaJ-like protein	4545242	503	GACCTGCTGTCCA GTTG [1952]	AATTCACGGGTTTTTC TCG [1953]
44	<i>OriX</i>	Regulatory protein, glycerol metabolism	1399486	472	ATGGATGCTCGGG TACTG [1890]	CTCAGCTACAGCCAC GAC [1891]
45	<i>pa026 0</i>	Hypothetical protein	15595198	473	GATCGTCTCTGCCC AGTC [1892]	ACATTGATGGTGTGCG TCC [1893]
46	<i>pa057 2</i>	Hypothetical protein	15595198	474	AGGAGAGAACATG AGTCGC [1894]	TCCTTGTCCCAGTAG TTACC [1895]
47	<i>pa104 6</i>	Hypothetical protein	15595198	477	AGGCATCCATCGA GCTAC [1900]	AACGTCCGAGCAGG ATAC [1901]
48	<i>pa106 9</i>	Hypothetical protein	15595198	478	GCGAGGAGGTATT CGACA [1902]	CCCTTCTCGAGTAG TGTT [1903]
49	<i>pa184 6</i>	Hypothetical protein	15595198	479	AAGGACTTCTGGTC GGTG [1904]	CAGGAACAGGTGCT CGTAG [1905]
50	<i>pa408 2</i>	Hypothetical protein	15595198	481	CGAGCACCAATATC GAAC [1908]	GAGCCGTAGGTGTT ATCG [1909]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
51	<i>pchG</i>	Necessary for formation of siderophore pyochelin	4325021	504	CCTGCTCAACACCT TCTATC [1954]	GTCGAACAACGCCA ACAG [1955]
52	<i>PhzA</i>	Phenazine biosynthesis proteins (low molecular weight toxins)	5616088	505	GTTGAAAGGGTTTA CCGAC [1956]	AATTTCTGCATCGGG TTC [1957]
53	<i>PLC</i>	Phospholipase C (heat labile-hemolysin)	151492	507	GACTTCGCTGTTTG ACTTC [1960]	TCGGTTCGAGTTCAT AGC [1961]
54	<i>plcN</i>	Non-hemolytic phospholipase C	151497	508	GTGTTCCAGGTGTT CGAC [1962]	GATAGACGTTGTCTT TGACC [1963]
55	<i>plcR</i>	Phospholipase C regulation	151499	509	ACAACTGGAACA GCAACT [1964]	CGACTCTTGGCGGTA TTC [1965]
56	<i>PstP</i>	Phosphoenolpyruvate-protein phosphotransferase	4545246	485	GAAGTGAACTCGG CCAAAG [1916]	TCGAGCATCATCAGG TAGAC [1917]
57	<i>purK</i>	AI/R carboxylase II, purine biosynthesis	1621599	486	TCGAGAAAGTCGAT GTTCAAG [1918]	CTTGCCGTAAGTGATG CAG [1919]
58	<i>rhlA</i>	Rhamnosyl-transferase involved in rhamnolipid biosynthesis	452502	518	AGTCTGTTGGTATC GGTTTG [1982]	CTCCAGGTCGAGGA AATG [1983]
59	<i>rhlR</i>	Rhamnolipid regulation	1117916	520	TTCGATTACTACGC CTATGG [1986]	GGTCCATTGCAGGAT CTC [1987]
60	<i>toxA</i>	Exotoxin A precursor	15595198	522	GTGCGCTACAGCT ACACG [1990]	CTTGCCCTCCAGGT ATC [1991]
61	<i>uvrDII</i>	DNA helicase	3249556	487	AGACCTACAACAAG GTTTCG [1920]	TGAGGATAGTCCCTT CGC [1921]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward[SEQ ID NO]	Primer reverse [SEQ ID NO]
62	<i>vsmI</i>	Autoinducer synthesis protein	695153	488	ATTCTCTCTGAAT CGCTG [1922]	AATATCTTCATCGCC AGTTG [1923]
63	<i>xcpX</i>	Secretion protein, translocation of exoproteins across outer membrane	45433	490	TTCAACCTCAACGG ACTG [1926]	TGCAAGGTACTCACC AGC [1927]
64	<i>ExoS</i>	Exoenzyme S, secreted toxin	13892017	497	CGTTTGGGACAGA TTGAG [1940]	GATACTCTGCTGACC TCGC [1941]
65	<i>fpvA</i>	Ferripyoverdine receptor	1633044	498	AATGCGATAACCAT CAGC [1942]	CCGTCGTA CTGGAA GTTG [1943]
66	<i>pa0625</i>	Hypothetical protein	15595198	475	AGGAGCAACTGAA GCGAC [1896]	TCTGCCCTTTACCCAG GAC [1897]
67	<i>pa0636</i>	Hypothetical protein	15595198	476	AAGGTTGGCAGGA TCAAC [1898]	CTAGTGGCGAAAATTG AACAG [1899]
68	<i>pa3866</i>	Hypothetical protein	15595198	480	TTCCCTAACGAATG CTGTC [1906]	CGTTGCTCCCTCATA CAC [1907]
69	<i>PhzB</i>	Phenazine biosynthesis proteins (low molecular weight toxins)	5616088	506	ATGCTCGATAATGC TATTCC [1958]	TTCTCGTAGTAACCC TCGG [1959]
70	<i>pilAp</i>	Type IV pilin, involved in twitching motility and attachment	18535593	482	GCTTTACCTTGATC GAACTG [1910]	TCAATAGAGCCAGTC ACACC [1911]
71	<i>PilAp2</i>	type IV pilin, involved in twitching motility and attachment	21629637	483	TGCCGTGAGTGAA ATCAG [1912]	CGTAGTTGGCTTTCC AGTT [1913]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
72	<i>pilC</i>	Pilin biogenesis protein	18535591	484	GGTATCAACCCACT AAAGGTC [1914]	GTCCAGAGCCTTCTAC CAGAG [1915]
73	<i>pvdD</i>	Pyoverdine synthetase D (siderophore)	1633044	510	GTCAAGGGTGTTG TCTGC [1966]	CTCTGCACAAACTCA GGG [1967]
74	<i>pyocin S1</i>	PyocinS1, bacteriocin	286179	512	CTTCAGTTCGAGA TGCC [1970]	GTAACGAACGCTATC GGG [1971]
75	<i>pyocin S1im</i>	Immunity protein of pyocin S1	286179	513	ATATACGGAAAAAG AGTTTCTTGAG [1972]	AGCACGCCATTCTTT AACTTC [1973]
76	<i>pyocin S2</i>	PyocinS2	286182	514	TATACGGCTTCAGA CTTTCC [1974]	TGGCATAAGTATTGG CAG [1975]
77	<i>pys2(1)</i>	PyocinS2	15595198	515	TCGCCAATAAGAAAG AAATTG [1976]	AGTGGTACTCGAAG GGTTCT [1977]
78	<i>pys2(2)</i>	PyocinS2	15595198	516	ATCCAGTATATTCC TGCTCG [1978]	TGCAATTTCTTCTTAT TGGC [1979]
79	<i>rfb303</i>	B-band LPS (O-antigen) biosynthesis	836903	517	ATCGTTCTGGTCTT CCTTG [1980]	ACCAAAGAGTGTTGA TAGCC [1981]
80	<i>rhlB</i>	Rhamnosyl- transferase involved in rhamnolipid biosurfactant synthesis	452502	519	AACGCTTCTTCGAT CAGG [1984]	GATACTGTGCGGTTG TGA [1985]
81	<i>femA</i>	Factor essential for methicillin resistance	4929298	801	TACAGTCATTTCAC GCAAAAC [2548]	TCACGCTCTTCATTT AGTTCT [2549]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
82	<i>fmhA</i>	Factor essential for methicillin resistance	4574232	825	TGACTTCGGATGA GTTCAT [2596]	GCTGTTAATTGTTGT TGCTTT [2597]
83	<i>fmhB</i>	Factor essential for methicillin resistance, putative	4574234	818	CTCACCCAAATGGA GATTTA [2582]	CTTGCTTTTCAGATG TTTCC [2583]
84	<i>gyrA</i>	DNA gyrase subunit A	296393	60	AGGCTCGTATGATT GAAAA [1066]	GGTTTTGAGCACGAT ATGTAG [1067]
85	<i>gyrB</i>	DNA gyrase subunit B	296393	61	TTGGCACAACTGAT AAGACA [1068]	AAAAATCGTTCAAAG TGCTC [1069]
86	<i>hemB</i>	Porphobilinogene synthase	2589180	62	ATCATCAGCGACAA TGAGAG [1070]	TTTTAAACATCTCGA ACTATATCTAA [1071]
87	<i>hemN</i>	Oxygen-independent coproporphyrinogen oxidase	14349226	65	TCTTCCATTCTCTC AGTCAAA [1076]	AGACCATGTATGTAG GTGGC [1077]
88	<i>hla</i>	α -Hemolysin	46763	120	GTCAGCTCAGTAAC AACAAACAC [1186]	GTAGCGAAGTCTGG TGAAAA [1187]
89	<i>lip</i>	Lipase	393265	68	TGCATCTTCCATTT TAATAGC [1082]	GTCATTGTCCTTTGT TGGTT [1083]
90	<i>menC</i>	o-Succinyl-benzoic acid synthetase	1255258	69	TTGACAGCTTTGCA TTTTTA [1084]	GGCTTTGTTGCTTTT AATGA [1085]
91	NAG	N-acetyl-glucosaminidase	2506026	125	AAGTTGCTCAAATA CAAGCTG [1196]	TGATGTTAGCCCAAT CTACA [1197]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
92	<i>norA2 3</i>	Quinolone resistance protein	4115706	904	GGTACTTGTTGCT GCTTTT [2754]	CGTAATCGCAATCGA AATA [2755]
93	<i>nuc</i>	Nuclease	46623	71	TGGCTATCAGTAAT GTTTCG [1088]	GAATCAGCGTTGTCT TCG [1089]
94	<i>rpoB</i>	RNA polymerase B- subunit	677848	73	TGGAAGACATCGT AAACGTA [1092]	TGGATCAAAGAAACG TGAAT [1093]
95	<i>tag</i>	DNA- 3-methyladenine glycosidase	6434027	81	TTTTGATTATCTTC TGACGG [1108]	CATTCAATTTATTCCC ACCT [1109]
96	<i>16SSa</i>	16S rRNA	46498	942	TCTCTGATGTTAGC GGCGG [2830]	TCAGGCTTTTCGCCCA TT [2831]
97	<i>clfB</i>	Clumping factor B	3393010	4	TAGCATAGCAACAA ACAGTGA [954]	GTTTTGACCTGAAGC TGTATC [955]
98	<i>EDIN</i>	Epidermal cell differentiation inhibitor	152997	113	AAAGATAGTTCTAA GATAAATGGTC [1172]	GGCCATTATTGGTCT GTTG [1173]
99	<i>elkT-abcA</i>	Lantibiotic epilancin K7 translocator	1841513	896	ATTAGAAATTGCGA CTGGTG [2738]	AGCGTGTCAATATCCT TCATC [2739]
100	<i>epiP-bsaP</i>	Biosynthesis of lantibiotic epidermin; serine protease	21204850	58	CTTAGATGTCCCAT GCTGAT [1062]	GTCAAACGAGTGCTA ATGGT [1063]
101	<i>geh</i>	Lipase precursor; glycerol ester hydrolase	153019	59	TTCAATAGGCGTG GTGTC [1064]	TTATCTGTCGGTTTC TCTGG [1065]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
102	<i>mreA</i>	ABC transporter	7548683	907	TACGATGACACCA GTCTTTG [2760]	ATCGACAAAACGTAC AGGAT [2761]
103	<i>murC</i>	UDP-N-acetylmuramoyl- L-alanine synthetase	2642658	70	GTATTATTGCTTGG GGTGAT [1086]	GGATAATTCCTTCGT GCTGT [1087]
104	<i>sak</i>	Staphylokinase	47425	126	TGTTATTATTCTCA TTTTCTTCAAT [1198]	ATGCTCTGATAAATC TGGGA [1199]
105	<i>sea</i>	Enterotoxin A	153120	127	TTTTATTGCTGCG CTAACG [1200]	TTTTAGAGTTAATC GTTTTATTATC [1201]
106	<i>sec1</i>	Enterotoxin C	46566	129	AATTTTGGCACAT GATTTA [1204]	CTTTATGTCTAGTT CTTGAGCTG [1205]
107	<i>eitb</i>	Exfoliative toxin B precursor	15301	115	TTTTAGCAGCGTCA ATTTTT [1176]	CTGATCCAGAGTTTC CTACCT [1177]
108	<i>seb</i>	Enterotoxin B	152999	128	CGTAGATGTGTTTG GAGCTA [1202]	CTTGAGCAGTCACCT TTTTTC [1203]
109	<i>ssfC</i>	Iron transport protein	3724154	80	TGATATTGGAAGAT ATTAGCATAGA [1106]	TGACAATCGCTTTAT TCATTT [1107]
110	<i>tst</i>	Toxic shock syndrome toxin	18266750	138	TTTTTATCGTAAGC CCTTTG [1222]	CAATAACCACCCGTT TTATC [1223]
111	<i>aacA-aphD</i>	Bifunctional aminoglycoside modifying enzyme	3676412	843	AGATTTGCCAGAAC ATGAAT [2632]	TGTTGCATTTAGTCT TTCCA [2633]

(continued)

Array No.	Symbol	Function	gi number	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
112	<i>aadD</i>	Aminoglycoside acetyl transferase	21623792	837	GCTATTGGTGTTTA TGGCTC [2620]	CTGATTGCTTAACTG CTTCA [2621]
113	<i>aph-A3</i>	3'5'-aminoglycoside acetyl-transferase	1272325	840	GAGAATATCACCG GAATTGA [2626]	GCTCGACATACGTGT CTTCC [2627]
114	<i>blaZ</i>	β -lactam ase	1575124	827	TGCTTTAGTTTTAA GTGCATGT [2600]	TCCTTCATTACACTC TTGGC [2601]
115	<i>cat</i>	Chloramphenicol acetyl-transferase	46651	862	AGAAAAATTGGGATA GAAAAGAA [2670]	CTGCAAGGCAACTG GTAT [2671]
116	<i>dhfrA</i>	S1 dihydrofolate reductase	3676404	859	CAATTACCTTGGCA CTTACC [2664]	CCCTTTTCTACGCAC TAAAT [2665]
117	<i>ermA</i>	rRNA methylase	13785452	852	CCAGAAAAACCCTA AAGACA [2650]	AAAGAACACGATATT CACGG [2651]
118	<i>ermC</i>	Adenine methylase	4138444	846	ACACAGTCAAAACT TTATTACTTCA [2638]	CAACAAGTTTATTTT CTGTAGTTT [2639]
119	<i>msrSA</i>	Macrolide antibiotic resistance	3892641	854	GACAGATTTTCGAT CCCTTA [2654]	CCTTTTGTTTTGAT GCACT [2655]
120	<i>mecA</i>	Penicillin binding protein 2'	13785452	802	AGTTGTAGTTGTCG GGTTTG [2550]	TGAAGTCGCTTTTCC TAGAG [2551]

[0098] *S. aureus*, *E. coli* and *P. aeruginosa* genes were selected from the literature and databases, and compared by BLAST analysis to all other sequences available in the NCBI database. Primers were designed to amplify gene segments of 200-810 bp length and devoid of apparent homology with genes of other bacterial species and *Homo sapiens*. Gene segments were amplified by using the puReTaq Ready-To-Go PCR beads (Amersham Biosciences, Freiburg, Germany) and cloned into the pDrive Cloning Vector (Qiagen, Hilden, Germany) according to the recommendations of the suppliers and transformed into competent *Escherichia coli* (XL-1-Blue) cells using the calcium chloride protocol (Sambrook, J., Russel D.W., Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, NY (2001)).

[0099] For quality control purposes, all gene probes were partially sequenced and verified (with the BigDye kit 1.1 and an 377 DNA sequencer; Applied Biosystems, Foster City, USA). All sequences obtained were identical or substantially identical (>90% sequence identity) to those obtained from the database.

[0100] For DNA-probe production 120 recombinant plasmids containing *S. aureus*, *E. coli* and *P. aeruginosa* gene segments were used for re-amplification. Amplicons were purified and spotted in 4 replicates per slide on UltraGAPS™ Coated Slides (gamma amino propyl silane coated slides, Corning, NY, USA). Approximately 1 nl DNA (with a concentration of about 0.1 to about 0.2 ng/nl) per spot was spotted onto the slide with a Biorobotics Microgrid Microarrayer (Genomic Solutions, Ann Arbor, MI, USA).

Example 5: Hybridisation and scanning

[0101] All experiments described represent dual co-hybridisations of two different target DNA samples labelled respectively with Cy3, Cy5 or Alexa647. After removal of unbound label, Cy3 and Cy5/Alexa647 labelled DNAs were pooled and mixed with 10 µg of Salmon Sperm DNA and 50 µg of poly-A-DNA. The mixture was frozen in liquid nitrogen and lyophilised in the dark. Prior to hybridisation the target DNA was reconstituted in 33 µl H₂O and 55 µl 2x hybridisation solution (Memorec Biotec GmbH, Cologne, Germany) and chemically denatured with 11 µl denaturation buffer D1 (Mirus) and neutralized with 11 µl buffer N1 (Mirus) according the instructions of the supplier. Hybridisation was automatically performed with a TECAN Hybridisation Station (HS400, TECAN, Salzburg, Austria). The arrays were prewashed at 60 °C for 1 min with 0.2% SDS and 4x SSC and prehybridised in 120 µl denatured prehybridisation buffer (Memorec) for 30 min at 60 °C at mild agitation. After injection of 110 µl labelled DNA, hybridisation was performed at 60 °C for 18 hours at mild agitation. The arrays were washed at 50 °C in primary wash buffer (Memorec) - five cycles of 1 min wash time and 30 s soak time - and in secondary wash buffer (Memorec) - five cycles of 20 s wash time and 30 s soak time -, and finally dried at 30 °C with N₂ (2.7 bar) for 3 min. Hybridised arrays were scanned with a Scan Array 5000 laser scanner (PerkinElmer). Laser light of wavelengths at 532 and 635 nm was used to excite Cy3 dye and Cy5/Alexa647 dye, respectively. Fluorescent images were analysed by the ImaGene software (BioDiscovery, El Segundo, CA, USA).

Example 6: Specificity

[0102] In order to allow the simultaneous and rapid identification of *S. aureus*, *E. coli* and *P. aeruginosa* grown in blood culture specimens from septicemic patients, a microarray comprising a set of 40 *S. aureus*, 31 *E. coli* and 49 *P. aeruginosa* gene probes of 200 to 810 bp length was developed (Tab. 2).

[0103] The specificity of the DNA-chip was validated firstly (compare Example 1) with 45 well characterised clinical isolates and reference strains of the three target species as well as other related bacteria and secondly (compare Example 2) with 13 blood cultures from sepsis patients.

[0104] In all assays, three PCR-amplified DNA-segments, which had been added to each DNA preparation as a positive control, hybridised with the corresponding probes, indicating that labelling and hybridisation had performed efficiently.

[0105] Hybridisation experiments with *S. aureus*, *E. coli* and *P. aeruginosa* target DNAs, respectively, revealed specific hybridisation with the species-specific gene probes (Fig. 1). There was no cross-hybridisation between the three species with the exception of the *S. aureus* 16S rRNA gene probe (16SSa, Fig. 1 C), which hybridised also with *E. coli* and *P. aeruginosa* target DNA.

[0106] Identification of *E. coli*, *P. aeruginosa* and *S. aureus* reference strains, clinical isolates and blood cultures (BC) by microarray analysis corresponded by 100% with the conventional identification results (Fig. 1).

Example 7: Detection and discrimination

Example 7A: Detection and discrimination of *E. coli*

[0107] All DNA samples from 9 *E. coli* strains hybridised always with seven *E. coli* gene probes (*envZ*, *fes* (1) and (2), *nfrB*, *yacH*, *yagX*, *ycdS*) (Fig. 1 A, columns 19 to 27); in the following these genes are designated as core genes.

With 14 *E. coli* gene probes variable hybridisation was observed including the antibiotic resistance gene probes *bla-TEM106*, *sul*, *strB* and *aacC2*. Such a variable hybridisation profile is expected for antibiotic resistance genes since acquired resistance to antimicrobials is strain specific. For 11 *E. coli* virulence gene probes (*eae*, *eltB*, *escR*, *escT*, *escU*, *espB*, *hlyA*, *hlyB*, *SLTII*, *toxA-LTPA*, *VT2vaB*) no hybridisation signals were detected with any of the tested *E. coli* isolates and blood cultures. Since these virulence genes are known to be specific for particular *E. coli* pathotypes (Bekal, S. et al., J. Clin. Microbiol., 41:2113-25 (2003)), it was not surprising that they were not present in the tested strains. The *eae*, *esc* and *esp* genes for example are encoded on a chromosomal pathogenicity island, which is typical for enteropathogenic *E. coli* exhibiting the unique virulence mechanism known as attaching and effacing (AE) (Elliott, S.J. et al., Mol. Microbiol., 28:1-4 (1998)). The alpha-hemolysin (*hly*) operon is encoded on a large plasmid of enterohemorrhagic *E. coli* strains (Schmidt, H. et al., Infect. Immun. 63:1055-61 (1995)).

Example 7B: Detection and discrimination of *Pseudomonas aeruginosa*

[0108] DNA samples obtained from *P. aeruginosa* uniformly hybridised with 32 out of 49 *P. aeruginosa* specific gene segments including the *mexA* gene probe (core genes). Variable hybridisation was observed with 17 probes allowing for discrimination of individual *P. aeruginosa* isolates (Fig. 1 B, columns 12 to 18).

Example 7C: Detection and discrimination of *S. aureus*

[0109] Hybridisation experiments performed with 11 *S. aureus* target DNAs revealed signals in all assays with 16 *S. aureus* gene segments (core genes) (Fig. 1C, columns 1 to 11). Variable hybridisation was observed with 14 *S. aureus* gene probes including the 6 antibiotic resistance gene segments *aadD*, *aacA-aphD*, *blaZ*, *dfrA*, *ermA* and *mecA* and the virulence genes *sak*, *sea*, *sec1* and *EDIN*. The gene probes *geh*, *mreA*, *clfB* and *elkT-abcA* hybridised with 8, 10 (*mreA* and *clfB*) and 6 target DNAs respectively. However, PCR amplification of the four genes was positive for all 11 *S. aureus* target DNAs (not shown) suggesting that the four genes were present in all strains investigated and that these gene probes did not allow reliable detection of the four genes in *S. aureus*.

[0110] No hybridisation was observed with 10 probes including the toxin genes *seb*, *tst* and *etb*. In contrast to the community-acquired, multi-susceptible MRSA strain MW2 that hybridised to *mecA* and *blaZ* only, all six clinical MRSA strains showed the same multiresistant hybridisation pattern and their DNA hybridised to *ermA* (erythromycin resistance), *mecA* (oxacillin resistance) and the *aadD* gene (tobramycin resistance). As for the majority of multiresistant MRSA strains the *ermA* and *aadD* genes were shown to be located upstream and downstream, respectively, of the *mecA* gene in the *mec* chromosomal region (Chambers, H.F., Clin. Microbiol. Rev., 10:781-91 (1997); Polyzou, A. et al., J. Antimicrob. Chemother., 48:231-4 (2001)). Hybridisation to the core gene probes permitted the identification of *S. aureus*, while hybridisation to antibiotic resistance gene probes allowed for discrimination of strains.

Example 7D: Discrimination of *E. coli*, *P. aeruginosa* and *S. aureus* from related bacterial species

[0111] Co-hybridisation experiments performed with related bacterial species confirmed the high specificity of the DNA-chip (Fig. 1): For *S. epidermidis* and all other Coagulase-negative staphylococci, cross-hybridisation was observed only with the *S. aureus* 16S rRNA gene probe (16SSa, Fig. 1 C) and several common staphylococcal antibiotic resistance determinants (*aadD*, *aacA-aphD*, *aph-A3*, *blaZ*, *cat*, *dfrA*, *ermA*, *ermC*, *mdrSA*, *mecA*) (Fig. 1C, columns 28 to 36). There was no cross-hybridisation with other metabolic or virulence genes of *S. aureus*.

[0112] The *Micrococcus* spp. isolate showed no hybridisation with the DNA-chip (column 53). Streptococci (column 56 to 58) and enterococci (columns 54 and 55) showed hybridisation with the staphylococcal 16S RNA gene probe and once with the staphylococcal *aph-A3* aminoglycoside resistance gene probe (*Enterococcus* spp.) (Fig. 1C). Out of 12 strains of seven Gram-negative species (columns 41 to 52), two hybridised with the *S. aureus* 16S rRNA gene probe (*Klebsiella pneumoniae* and *Proteus mirabilis*, Fig. 1C, columns 41 and 47) and one clinical isolate of *Proteus mirabilis* hybridised with the *E. coli* resistance genes *bla-TEM106* (β -lactam resistance), *sul* (sulfonamide resistance) and *strB* (streptomycin resistance) (Fig. 1A, column 42). *Serratia*, *Stenotrophomonas*, *Acinetobacter* and *Enterobacter* species showed no cross-hybridisation with any gene probe.

Example 8: Sensitivity

[0113] While the majority of *P. aeruginosa* probes allowed unambiguous identification, some probes showed variable hybridisation patterns when microarray hybridisation was performed with different target DNA samples prepared from the same isolate (Tab. 3).

Tab. 3: Microarray hybridisation signals obtained with different target DNA preparations of *Pseudomonas aeruginosa* isolates.

Isolate									
C4242				C3853		C3045		C3755	
DNA amount [ng]	130 ^a	382 ^a	1350 ^b	510 ^a	> 2400 ^b	550 ^a	2950 ^b	1180 ^b	> 1600 ^b
BDR ^c	22	75	48	29	30	90	41	139	40
No. of hybridised gene probes ^d	38 (88%)	31 (72%)	43 (100%)	36 (88%)	41 (100%)	34 (89%)	38 (100%)	41 (95%)	43 (100%)

^a Labelled with Alexa647

^b Labelled with Cy3 or Cy5

^c BDR: Base to dye ratio; number of nucleotides per one dye molecule

^d Number of signals obtained with *P. aeruginosa* capture probes (total 49) after hybridisation with different DNA preparations. The percentage of specific hybridisations is compared to the highest number of signals obtained for each isolate (100%).

[0114] Successful hybridisation with strong fluorescent signals depends on efficiency of DNA labelling (ratio of bases per one dye molecule) and amount of labelled DNA. For the different target DNA preparations of four clinical isolates, variable hybridisation was observed with 14 gene probes (*uvrDII*, *vsml*, *pa1069*, *rhIR*, *rhIA*, *rhIB*, *1046*, *pyocinS*, *pyocinS1im*, *plcR*, *plcN*, *PHZb*, *rbf303* and *pIIAp2*). For example, for three different DNA preparations of isolate C4242, hybridisation to *Pseudomonas*-gene probes varied from 31 to 43 probes, respectively, depending on the labelling efficiency and amount of DNA (Tab. 3). The lowest number of signals was detected with 382 ng target DNA, that, however, showed a high base to dye ratio of 75. Overall, the results suggest that varying amounts of DNA and base to dye ratios influenced the hybridisation results of few gene probes. However, irrespective of the varying quality and quantity of the labelled target DNA, 35 of the 49 *P. aeruginosa* gene probes showed robust hybridisation results in all performed experiments.

Example 9: Detection and characterisation of pathogens in blood cultures

[0115] Although DNA prepared from blood cultures comprises a mixture of human and bacterial DNA, the resulting hybridisation signals obtained with DNA from 1 ml positive blood culture allowed a clear and unambiguous characterisation of *S. aureus*, *E. coli* and *P. aeruginosa* present in 13 tested blood specimens (Fig. 1). In accordance to the VITEK2 characterisation, positive BACTEC® cultures were identified by microarray hybridisation as multi-resistant MRSA (Fig. 1C, column 8), penicillin-resistant *S. aureus* (column 9 and 11), multi-susceptible *S. aureus* (column 10), *E. coli* (Fig. 1A, columns 26 and 27), *P. aeruginosa* (Fig. 1B, column 18), and discriminated from oxacillin resistant *Staphylococcus epidermidis* (columns 33-35), *Proteus mirabilis* (column 43) and *Streptococcus pneumoniae* (columns 57 and 58).

Example 10: Correlation between susceptibility testing and microarray hybridisation of selected antibiotic resistance genes

[0116] *S. aureus*: For 11 *Staphylococcus aureus* strains and blood cultures, susceptibility results determined by the VITEK2 system, Etest strips and disk diffusion tests were compared with the results of the microarray hybridisation assay for the simultaneous detection of antibiotic resistance genes (Tab. 4). The presence or absence of resistance genes as indicated by microarray hybridisation was confirmed by PCR with gene specific primers (results not shown).

Tab. 4: Correlation between phenotypic and genotypic antibiotic resistance for 11 *S. aureus* isolates and blood cultures.

a) Penicillin resistance ^a	Hybridisation with <i>mecA</i> / <i>blaZ</i>	
	No. pos.	No. neg.
10 (resistant)	10	0
1 (susceptible)	0	1

(continued)

5	b) Oxacillin resistance	Hybridisation	with <i>mecA</i>
		No. pos.	No. neg.
	7 (resistant)	7	0
	4 (susceptible)	0	4
10	c) Erythromycin resistance	Hybridisation with <i>ermA</i> , <i>ermC</i> or <i>msrA</i>	
		No. pos.	No. neg.
	6 (resistant)	6	0
	5 (susceptible)	0	5
15	d) Tobramycin resistance	Hybridisation with <i>aadD</i>	
		No. pos.	No. neg.
	5 (resistant)	5	0
	6 (susceptible)	0	6
20	e) Gentamicin resistance	Hybridisation with <i>aacA-aphD</i>	
		No. pos.	No. neg.
	0 (resistant)	0	0
	11 (susceptible)	0	11
25	f) Trimethoprim resistance	Hybridisation with <i>dfrA</i>	
		No. pos.	No. neg.
	1 (resistant)	0	1 ^b
	10 (susceptible)	0	10
^a Number of strains tested for resistance			
^b <i>dfrA</i> gene detected by PCR			

[0117] For the *S. aureus* strains there was a 100% correlation between phenotypic resistance to penicillin and hybridisation to the *mecA* and/or *blaZ* gene (both genes confer resistance to penicillin, Tab. 4a). Phenotypic resistance to oxacillin correlated 100% with the hybridisation of the *mecA* gene (Table 4b), between resistance to erythromycin and hybridisation to the erythromycin resistance genes *ermA*, *ermC* or *msrA* (Tab. 4c) and between resistance to tobramycin and hybridisation to the *aadD* gene (Tab. 4d). Furthermore, they all showed 100% correlation between phenotypic susceptibility to gentamicin and no hybridisation to the resistance genes *aacA-aphD* (Tab. 4e). Notably the *dfrA* gene of the trimethoprim resistant strain MW2 (MIC of 1 µg/ml) was not detected by microarray hybridisation (Tab. 4f), whereas PCR amplification revealed the presence of the *dfrA* gene.

[0118] *E. coli* and other Gram negative bacteria: The prototype microarray harboured only four *E. coli* and one *P. aeruginosa* resistance gene probes which do not yet allow a comprehensive prediction of antibiotic resistances. Nevertheless, hybridisation with the *E. coli* resistance gene probe *blaTEM106* was observed in one *P. mirabilis* and four *E. coli* strains and correlated with phenotypic ampicillin resistance for all five strains (Tab. 5).

Tab. 5: Correlation between ampicillin/penicillin resistance, gentamicin/tobramycin resistance and streptomycin resistance and hybridisation with the resistance gene probes *blaTEM-106*, *aacC2*, *aph-A3* and *strB*, respectively.

Species	Resistance phenotype ^a	Hybridisation with			
		<i>blaTEM-106</i> ^b	<i>aacC2</i> ^b	<i>aph-A3</i> ^c	<i>strB</i> ^b
<i>E. coli</i> ATCC 25922	susceptible	-	-	-	-
<i>E. coli</i> C4821	AMP, STR	+	-	-	+
<i>E. coli</i> F3437	AMP	+	-	-	-
<i>E. coli</i> C3941	AMP, STR	+	-	-	+
<i>E. coli</i> F1806 ^d	AMP, GEN, TOB, STR	+	+	+	+
<i>E. coli</i> C4547	AMPi	-	-	-	-
<i>E. coli</i> C4230	AMP	-	-	-	-

(continued)

Species	Resistance phenotype ^a	Hybridisation with			
		<i>bla</i> TEM-106 ^b	<i>aacC2</i> ^b	<i>aph-A3</i> ^c	<i>strB</i> ^d
5 <i>E. coli</i> C3940	susceptible	-	-	-	-
<i>E. coli</i> F1642 ^d	STR	-	-	-	+
<i>P. mirabilis</i> C4024	AMP, STR	+	-	-	+
10 <i>P. mirabilis</i> C4403	susceptible	-	-	-	-
<i>P. mirabilis</i> F1738	susceptible	-	-	-	-
^a AMP, ampicillin; GEN, gentamicin; STR, streptomycin; TOB, tobramycin; i, intermediate					
^b <i>E. coli</i> gene probes					
^c <i>S. aureus</i> gene probes					
^d Positive blood culture					

[0119] One *E. coli* blood culture showed also resistance to tobramycin and gentamicin. This phenotypic resistance correlated with the hybridisation of the *aacC2* gene probe for aminoglycoside resistance and the *S. aureus aph-A3* probe for tobramycin/kanamycin resistance (Tab. 5). For one *P. mirabilis* and four *E. coli* strains, phenotypic resistance to streptomycin correlated with hybridisation to the *strB* probe (Tab. 5).

[0120] All *P. aeruginosa* strains hybridised with the *mexA* gene probe (Fig. 1) and showed phenotypic resistance to tetracycline, trimethoprim/sulfamethoxazole, penicillins (ampicillin, mezlocillin) and cephalosporines (cefazolin, cefixime, cefuroxime). The *mexA-mexB-oprM* operon is a determinant for a three component efflux system responsible for intrinsic and acquired multiresistance in *P. aeruginosa* (β -lactams, fluoroquinolones, trimethoprim, sulphonamides, chloramphenicol and others) (Poole, K., Clin. Microbiol. Infect. 10:12-26 (2004)).

Example 11: Microarray for specific detection of *S. aureus*

A) Strains and Cultures

[0121] Reference strains and clinical isolates: The following bacteria were purchased from the American Type Culture Collection (ATCC, Manassas, Va.) or the Deutsche Sammlung für Mikroorganismen und Zellkulturen (DSMZ, Braunschweig, Germany) and were used for evaluation of the specificity of the microarray: *Staphylococcus aureus* (ATCC 29213), *Staphylococcus epidermidis* (ATCC 12228; ATCC 18610) *Staphylococcus saprophyticus* (ATCC 14953), *Escherichia coli* (ATCC 25922), *Pseudomonas aeruginosa* (ATCC 27853). Ten clinical MRSA (methicillin resistant *S. aureus*) isolates were obtained from the inventors' clinical routine microbiology laboratory.

[0122] Bacterial cultures: Bacterial strains and clinical isolates were plated either onto sheep blood or onto Mueller-Hinton agar from 50% glycerol stocks. One colony was then picked and transferred to 5 ml Luria-Bertani (LB) broth and cultured overnight at 37°C.

[0123] Blood cultures: Aerobic blood culture bottles (BACTEC® Plus aerobic, Becton Dickinson, Heidelberg, Germany) were inoculated with 100 CFU of *S. aureus* after adding 10 ml blood from healthy volunteers. A BACTEC® 9240 blood culture system (Becton Dickinson) - a continuous reading, automated, and computed system detecting the growth of microorganisms by monitoring CO₂ production - was used for incubation according to the manufacturer's recommendations. Bottles with a positive growth index were removed from the incubator, and an aliquot of 1 ml of the blood culture suspension was taken aseptically with a needle syringe. The aliquot was equally divided, with one part for subculture on agar plates and CFU determination, and one part for DNA isolation.

[0124] Additionally, in order to test the microarray upon real conditions, samples were collected from ten clinical positive blood culture specimens cultivated under the same conditions as described above. Six of them were positive for different *S. aureus* strains and four for other bacterial species (*Staphylococcus epidermidis*, *Streptococcus mitis*, *E. coli* and *Klebsiella oxytoca*). Blood culture aliquots of 500 µl were used for DNA preparation.

B) Generation of the *S. aureus* specific microarray

[0125] About 140 gene segments of *S. aureus* genes, but also a few of CoNS (SEQ ID NO: 177,178,179), were selected from the literature and nucleotide databases in order to cover different functional categories (virulence factors,

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species-specific metabolic and structural features, antibiotic resistance determinants). Tab. 6 provides the complete list of selected genes with gene symbol, gene function and SEQ ID NO of the segments.

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Tab. 6: Selected *S. aureus* genes, selected segments (SEQ ID NO) and primers used for segment amplification (SEQ ID NO)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>atl</i>	autolysin	99	AGCTGAGACGACACA AGATCAAA [1144]	TTATATTGCGTTTCAAGA GCTGC [1145]
<i>aroA</i>	3-phosphoshikimate 1-carboxyvinyl-transferase	84	ACCTTCAATATTGCGA TCC [1114]	TATTCCGATTATTAGGCG TAG [1115]
<i>aroC</i>	Chorismatsynthase	83	ATGAGATACCTAACAT CAGGAGAAATCA [1112]	GCTATTCTTCCATCTAATT TAGCATCATA [1113]
<i>aroE</i>	Shikimatehydrogen ase	95	GTTATCAATTAATACA ACCCCTGAAGC [1136]	TGGAACATAATTCTCCTTC GATTGTTA [1137]
<i>aroF</i>	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase	96	GTAGTTGAAAAATATG CCTGTTGGTGT [1138]	ATTACACCATTAAACGATA ATTGGCAT [1139]
<i>aroG</i>	Chorismat-Mutase	97	AGACTTATTATCTAAA CGTGGTGAACCTAGC [1140]	CAAATGATTATTGCGCGT CTCCTA [1141]
<i>asp23</i>	alkaline shock protein	98	AAAATTGCTGGTATC GCTGCA [1142]	GTCATTACATCATCAACTT GCATGTTA [1143]
<i>catal</i>	catalase	1	TAAATTGTTTAGATTA CAATCAGAGG [948]	TTCAAAAGTTTTTCGATGTT TCA [949]
<i>clpC</i>	endopeptidase	7	AATGCTGCTAACCTG CGTGAT [960]	CACGTCIAACCGCTTTAC TGATTG [961]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>clpP</i>	endopeptidase	8	AAAGTAAAGAGTAGA CTAAGCTGTCTGCTC [962]	ACCTAATAAAATTCAAAGC ATTGGGA [963]
<i>ctaA</i>	cytochrome biosynthesis	9	AAGAATTTAAAATGGT TAGGTGTCGTA [964]	ACGTAATCGTTTTGTTC CAAATA [965]
<i>ctsR</i>	transcription repressor of class III stress genes homologue	10	AACGTCCCATGCCATT AATTTT [966]	TTGCGTTTCTATTTAGCTC AGACA [967]
<i>dltA</i>	D-alanine-D-alanyl carrier protein ligase	11	ACAGAGCAGCAAAAG CGTTAGTG [968]	GACCTTGAATGAACCATT GACCAT [969]
<i>dltB</i>	hypothetical membrane transporter	12	CATATGGTGATTTTAC ATTCTTCTTAATTG [970]	CCTAACCATGTACTTTGT AACACITTTCA [971]
<i>dltC</i>	D-alanyl carrier protein	13	AAATTTATTAGCAGAA GTAGCAGAAAATG [972]	CTGAACCTCTCTAATGCTT CAACGATT [973]
<i>dhak</i>	Heat-shock-protein	14	TTTAGGCGAAAATATT GGTGAAGA [974]	TTTGTGTCGTCCTTTTACT TCGTT [975]
<i>elk T</i>	lantibiotic eplancin K7 translocator	15	GGTCTTATCGTTGCA GCTATCACTAT [976]	GAGCGTATCGCATAAATA ATCTTTTC [977]
<i>eno</i>	2-phosphoglycerate dehydrogenase	87	CGATGTTTCATCATTGG TACTGGTA [1120]	GGTGTTACTAAAGCAGTT GAAAACG [1121]
<i>glnA</i>	glutamine synthetase; belongs to the fem C locus	17	TAGTCACCATGAAGTT GCCCC [980]	CCTCTTGAAGATGGTACA CGGAT [981]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>glnR</i>	glutamine synthetase repressor; belongs to the fem C locus	18	CGAATGATGCAATCA GACGAAA [982]	CACCACGATTTATTGGCA AAGTT [983]
<i>griA</i>	DNA topoisomerase IV subunit A	19	TTGAATCACCAAAATTG AGGTTGT[984]	CAGTCGTTCAGATTTGAA TTTTCTTT [985]
<i>griB</i>	gyrase-like protein beta subunit B	20	AAATCCATCGAGATG GTAATATATATCA [986]	AAACTTAAAAATACTTTCTG AATATTGATCAT [987]
<i>groEL</i>	stress response; heat shock protein	21	GTATGCAATTTGATCG TGGTTAT [988]	TGTTAATGCATCGCCTTC AAC[989]
<i>groES</i>	stress response; heat shock protein	22	ATGTATGTTAGCACTC TTTAATGTTAAGTG [990]	GTTTAGTTGTTTTCATTT TCGTT [991]
<i>gyrA</i>	DNA gyrase subunit A	60	CATCATTAAATTCGATT CCCTGAAT [1066]	TCATTTACTTCATCTGCAT CCTCTT [1067]
<i>gyrB</i>	DNA gyrase subunit B	61	TCAATTTGACTTAAAA GAAGTTGGC [1068]	AAGATTTGTGGCATATCC TGAGTTA [1069]
<i>hemA</i>	Glutamyl-transfer RNA reductase	23	TGTCATATTATCAACA TGTAATCGAACTG [992]	AATATCAGTAATTCAG ACCAAGAAGAT [993]
<i>hemB</i>	Porphobilinogene synthase	62	TTGATAGACATAGAA GATTGAGATCATCAG [1070]	ACTTGAGAAAATTGCTGTT TTAACAAGTAG [1071]
<i>hemC</i>	Porphobilinogene deaminase	63	GTAAATTAGTCGTTG GCTCCAGAAG [1072]	GGGATAGTGGTGATGTC TTTTAGAAATA [1073]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>hemD</i>	Uroporphyrinogen III synthase	64	TGTTGATAACATTGCT GTGATAGGAA [1074]	AATGCATCGATTGTTGA TGTTCTA [1075]
<i>hemE</i>	Uroporphyrinogen decarboxylase	24	AAAATGATCAAAAGGT GAAGAAACATC [994]	AATCCTCGACATTTAATG CACCTAC [995]
<i>hemH</i>	Ferrochelatase	25	AATGGGATTATTAGTT ATGGCTTATGG [996]	GTGGATATGGATCATTAT TCTTTTCG [997]
<i>hemL</i>	GSA-1-Aminotransferase	26	ATGAGATATACGAAAT CAGAAGAAAGCA [998]	CTAATCTTAAAGTATCCAA TGTAGCTTCIGTA [999]
<i>hemN</i>	oxygen-independent coproporphyrinogen oxidase	65	ACAGAATCAACCTGT AGATGAGTACTTAGA T [1076]	TGATATTCGTATAACGCA CACCATC [1077]
<i>hemY</i>	putative involved in a late step of protoheme IX synthesis	27	AAACAGCAAGATCCT AATATTGATGTAAC [1000]	CTCTACGTACAATCGATA CTAATTCATTATCT [1001]
<i>lepA</i>	GTP-binding protein	28	ATTAACAAAAATTGATT TACCTGCTGC [1002]	CTATAACCAAAACCTAAT GCTTGTGAC [1003]
<i>IrgA</i>	holin-like protein LrgA	29	AAAGACGCATCAAAA CCAGCA [1004]	GGCTAATGACACCTAAAG AGTTAACAACT [1005]
<i>IrgB</i>	holin-like protein LrgA	30	GATTAACCACTTAGCA CTAAACACACCT [1006]	AATGTTTAAACAAGCACTT CAGGCT [1007]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>lytM</i>	peptidoglycan hydrolase	31	CGACAAACACCCCAAC AAGCA [1008]	TGGCTGTTATACGCTTGG TTGT [1009]
<i>menB</i>	naphthoate synthase	32	GTTATCGTATTAACGTG GTGAAGGTGATT [1010]	ACATTTAGTACATTACCG CCACCTAC [1011]
<i>menC</i>	o-succinylbenzoic acid synthetase	69	TTTAAGTCACAAAATTG TAACACCGAA [1084]	TTAATTTAATTCTGGTCG GCTTTGT [1085]
<i>menD</i>	2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylase	33	CGTAAGGGAAGTAGT TATCAGTCCG [1012]	TTAGCTGTATACTCGAAA TCCAATCC [1013]
<i>menE</i>	O-succinylbenzoic acid-CoA ligase	34	ATGGACTTTTGGTTAT ATAAACAAAGCAC [1014]	TATTTCAGCAATGTCAAC CGTATTA [1015]
<i>menF</i>	Isochorismate-Synthase	35	ATTGATAATTTACATC CAACACCTGC [1016]	TCACTATCTGGATCAGAA TCTTTAACAAT [1017]
<i>murC</i>	UDP-N-acetylmuramoyl-L-alanine synthetase	70	CTTGGGGTGATGATG AACATCTA [1086]	AAGTGTGTGGTTGAAAATA CTGCAA [1087]
<i>mutL</i>	DNA mismatch repair protein	38	TCGTTTACATCATAAT AATCATCAGAC [1022]	ACACAGAGAATAACCAGG AGAAGA [1023]
<i>mutS</i>	DNA mismatch repair protein	39	TTGTAATTCAGCTTAAC TTCACCAATG [1024]	TCAAGTTGCGAAAATTAGC TGA [1025]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>pbg</i>	porphobilinogen synthase	41	GGTGTCCAAACTCA AAAGATGATATA [1028]	TTGACACCATAACTCATTA TAGGAATATTG [1029]
<i>pdhB</i>	pyruvate dehydrogenase (lipoamide): subunit E1beta	43	TGACATTTCAAATCAA TCACATCG [1032]	TTGGTAACCAAAACATTTTC AGCTT [1033]
<i>pdhC</i>	dihydrolipoamide acetyltransferase: subunit E2	44	CTGGAGATACTATTG AAGAAGACGATG [1034]	TTGCTTTTACAGTTCGTGT TTCATCTAC [1035]
<i>pdhD</i>	dihydrolipoamide dehydrogenase: subunit E3	72	CAGGTAAATTAGTTGT AGTTGGTGGAG [1090]	AGTGGTAAACCTGGAACG ATATCA [1091]
<i>rpoB</i>	RNA polymerase B-subunit	73	ATTGTTACGTGCATTA GGTTTCTCA [1092]	TTTCTACTGGCTCGTCTAT AACGC [1093]
<i>rsbU</i>	putative operon encoding alternate sigma factor	45	TAGTTATCGAGATTAT CAAAGATTGGTAGA [1036]	GTAATTGTGAGT GTCCAT AAGAATCCA [1037]
<i>rsbV</i>	putative operon encoding alternate sigma factor	46	TGAATCTTAATATAGA AACCAACCACTCAAG [1038]	ACGATCTGACACACCTAA AATGTA [1039]
<i>rsbW</i>	putative operon encoding alternate sigma factor	47	TCTAAAGAAGATTTTA TCGAAATG [1040]	CCCACATTGTTATTTTCTT TGTAT [1041]
<i>sdcC</i>	serine-aspartate repeat protein multigene family	139	GAAAGTATTCTGTAG GTACTGCTTC [1224]	CCTTTATCAATCGCAATG TC [1225]
<i>sdcD</i>	serine-aspartate repeat protein multigene family	140	CGGGCAAATAAATAA AGATG [1226]	AACTGAAGATAAGCCGTT TG [1227]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>sdrE</i>	serine-aspartate repeat protein multigene family	141	TCTGTCGCAGTTTTAT CAGTTGAAG [1228]	GCAAAACAAGATGATGCA ACG [1229]
<i>sgp</i>	G protein	48	TGAGATAGATGCAAT CATGTTTATGG [1042]	GAAATAGGTACAATCTCT GTAAAGTCCATATA [1043]
<i>sigB</i>	sigma factor B	78	GATGGTTCAACTGTTA CGCTATTA [1102]	CTCTGAAGTCGTGATACA TGCA [1103]
<i>sirR</i>	sit operon metal dependent repressor	49	AATATAATTGGGAAG AAGTACATCAAGAAG [1044]	ATATTAGCAAAATCGGTCT TATCTCTCA [1045]
<i>sodA</i>	superoxide dismutase	50	TTGAATTACCAAAATT ACCATACG [1046]	CTCCCAGAAATAATGAATG GTTTAAAT [1047]
<i>sodB</i>	superoxide dismutase	51	GCGCATTTTGAAAAG GCA [1048]	GGGATAGCACGTAAAAAGT GGAA [1049]
<i>srtA</i>	transpeptidase;sorta se that anchors surface proteins to the cell wall	91	CTGGTCCTGGATATA CTGGTTCITT [1128]	GATTAATGACAAATCGCTG GTGTG [1129]
<i>sstA</i>	iron transport proteins	52	TTCGTTGTTTCATAGGT GCGAGT [1050]	CTTTGAACAGCACACTCGTG CG [1051]
<i>ssfB</i>	iron transport protein	53	TATTGCCCTTATTAGA TGTATTGCTTTT [1052]	TCGTAGCTTCAAAACACAT TTTCAA [1053]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>sstC</i>	iron transport protein	54	AATCAAATGATATTGG AAGATATTAGCA [1054]	TATTCAGTATCTTGTGCTA TTGTCATTG [1055]
<i>sstD</i>	iron transport protein	55	CATGCGGTAAACAATT CTGATAAAGA [1056]	AATTTTCGCITTTAGGTGC AGCT [1057]
<i>stpC</i>	Potential ABC transporter	92	TTAACAAATAGAACATT TAACAAAGAAG [1130]	CTCGAAATTAAGAAAAGTA ACACC [1131]
<i>tag</i>	DNA-3-methyladenine glycosidase	81	GCATTTGGTACTAAA GATCCAGTCTACT [1108]	AACGAAAATACTGTTACT GGACCTAAAA [1109]
<i>trx</i>	thioredoxin reductase	56	GCTGACTATGAAGGT AAAGCTGACA [1058]	CAGCTAAGTTTTCTTTTG GTTGGA [1059]
<i>tyrA</i>	prephenate dehydrogenase	82	ATTCATTTAGTCAGTG GTCATCCAAT [1110]	GCTGTCGAATCATTCTA AAATATACGT [1111]
<i>yhiN</i>	yhiN-protein	57	CAATTGGCTTTCGATT ATTGTTGTA [1060]	AACCAATGATCTAGTGA AATGTTAAACCT [1061]
	Virulence Factors			
<i>clfA</i>	clumping factor A	3	GCTTCAGTGCTTGTA GGTACGTTAA [952]	TTGATTCACTAATTCCTCC GCAT [953]
<i>clfB</i>	clumping factor B	4	TAATGATACATCTGAT ATTAGTGCAAAACAC [954]	TTTAGCATCAGCAGCATT TACTACC [955]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>cna</i>	collagen adhesin	85	TCGAGGAATTAACAA AGGTC [1116]	ATCAGGTTTAGTTGGTGG TG [1117]
<i>coa</i>	staphylocoagulase	5	TGTTAGGGATACACA ACATAAAACTGA [956]	GATTTGTTTCAGATTTCAC CGTATTT [957]
<i>ebpS</i>	cell surface elastin binding protein	86	GACCTAGCCATCAA GACAG [1118]	GCATTATTAGAGGCATGT GG [1119]
<i>EDIN</i>	Epidermal cell differentiation inhibitor	113	TATCTTTAGCATTAAAG CGTTTATTCAAT [1172]	TTTCTAACTAGATTTTCAT CATACTGGC [1173]
<i>eta</i>	exfoliative toxine A precursor	114	TGCATTTAATTTACCA AAAGAGCTT [1174]	TGGATAGCCTATTAAATTC GAGTTTG [1175]
<i>etb</i>	exfoliative toxine B precursor	115	AAGAGCTTTATACACA CATTACGGATAA [1176]	CAAAATATTGAGAATCAT TGAACATTTTC [1177]
<i>fbpA</i>	fibrinogen binding protein	88	CTCTTTTACCTTTGA CGTTGGATT [1122]	GCCAAAATAGTGCTTCAA TATCAGA [1123]
<i>fib</i>	fibrinogen binding protein	89	GCTTTTCTGTGTGCAC TGACAGT [1124]	AGCGAAGGATACGGTCC AAG [1125]
<i>fnbA</i>	fibronectin-binding protein	93	TTACATCTGTACCCGT TTCCACTT [1132]	AAACTGCACAAACCAGCAA ATATAGA [1133]
<i>fnbB</i>	fibronectin-binding protein	90	CCGCCTTAATTCCTTC TCCAAA [1126]	GCGAGTTGATTGGCCATC GG [1127]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>geh</i>	lipase precursor; glycerol ester hydrolase	59	GAACAAGGGAATGCG ATAACG [1064]	AGGTGCAGTTTTATCATT AGACGG [1065]
<i>hla</i>	alpha-hemolysin	120	ATGATGAAAAATGAAA ACACGTATAGTC [1186]	ATTTGAGCTACTTCATTAT CAGGTAGTTG [1187]
<i>hlb</i>	beta-hemolysin	121	TGTTAATAAAGGCACT CCAGAGTTC [1188]	CTTTGATTGGGTAATGAT CTGAAAA [1189]
<i>hld</i>	delta-hemolysin	110	TTTTATCTTAATTAAG GAAGGAGTGATTTC [1166]	TAGTGAATTTGTTCACTG TGTCGATAA [1167]
<i>hlgA_C</i>	gamma-hemolysin component A; C-terminus	117	ACTGAAGTAGAAAAGT CAGAACTCTAAAGGT [1180]	GTGTTTTCCAGTTCACTTC ATATTTAACT [1181]
<i>hlgA_N</i>	gamma-hemolysin component A; N-terminus	116	CTTAAAAATTAATAGA AAGAAAGT [1178]	ATGTTTTGAGTTATAGCT AATCGTT [1179]
<i>hlgB</i>	gamma-hemolysin component B	118	ATAGCTTCCACCCAAC ATATGGTAA [1182]	ATTTCACTTTGTGATTTTC CCAATC [1183]
<i>hlgC_C</i>	gamma-hemolysin component C; C-terminus	119	AATCAGCATTGATAG CGATTTATTT [1184]	CCAATTGACTTCATATTC ACAGTGTA [1185]
<i>hysA</i>	hyaluronate lyase	111	AAACATCAAATCGCT GTGGCT [1168]	GTGAAAAGATGCCCTTGAG TGG [1169]
<i>lgGbg</i>	IgGbinding protein	112	GGGTTCTTGCTGTCTT TAAGTGATT [1170]	TATATCTCGAAGTTGCTA GTTGGGG [1171]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>lip</i>	lipase; glycerol ester hydrolase	68	TTTAAAGTGGTGGAC AAGCACAA [1082]	GATTGTTATTAGCGTTTG AATCTTGAC [1083]
<i>lukF</i>	leucocidin F	122	CATATGGCAGAGATA GTTATCATTTCAACT [1190]	GATGATGAGTTGCTCTT ATGTGATCTTTA [1191]
<i>lukS_C</i>	leucocidin S; C-terminus	124	AGTGTTCAATGGGA ATAAAAGCTA [1194]	GATCCTTCTAAATAACTAT TGCCATAGTG [1195]
<i>lukS_N</i>	leucocidin S; C-terminus	123	AACATTGTCGTTAGG AATAATCACT [1192]	AATCAAAGCATCTTTGTTA TACTTT [1193]
<i>NAG</i>	N-acetylglucosaminidase; cytotoxin	125	ACTCAAACAGTTAGC AAGATTGCTC [1196]	TGCATTTACCCCAACCAGT GC [1197]
<i>nuc</i>	nuclease	71	GCGATTGATGGTGAT ACGGTT [1088]	TTTTCGCTTGCTTCACT TTT [1089]
<i>sak</i>	staphylokinase	126	CGAGTTATTTTGAACC AACAGGC [1198]	GCGCAAAGATCGAAGTCA CTTAT [1199]
<i>sea</i>	staphylococcal enterotoxin A precursor	127	CTGATGTTTTTGATGG GAAGGTT [1200]	TGCATGTTTTTCAGAGTTA ATCGTTT [1201]
<i>seb</i>	staphylococcal enterotoxin B precursor	128	ATATATTCTATTAAGG ACACTAAGTTAGGGA AT [1202]	AGTTAGGTAATCTAATTCT TGAGCAGTCA [1203]
<i>sec</i>	staphylococcal enterotoxin C precursor	129	GGCACATGATTTAATT TATAACATTAGTG [1204]	ATTCCTAGCTTTTATGTCT AGTTCTTGAG [1205]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>spa</i>	immunoglobulin G binding protein A precursor	94	GGTATTGCATCTGTAA CTTTAGG [1134]	AGGTTAGCACTTTGACTT GG [1135]
<i>spv8</i>	V8 serine protease gene	137	ACAAACGCAGTCAAG CAACA [1220]	CATTGTTGCTGGTTTAAAC TACTTCAC [1221]
<i>tst</i>	toxic shock syndrom toxin	138	AAATTACCTACTCCA ATAGAAGTACCTTT [1222]	TTTCTGCTTCTATAGTTTT TATTCATCA [1223]
	Antibiotic Resistance Determinants			
<i>aacA-aphD</i>	bifunctional aminoglycoside modifying enzyme	843	CCCTCATAAAAATAA C CCAAGAGC [2632] T	CTTTTCTTTTGCATAAACC TTTTTTC [2633]
<i>aadD</i>	aminoglycoside acetyl transferase; kanamycin resistance	837	AAGCAGAGTTTCAGCC ATGAATG [2620]	CAGATGCGATGATGCAGA CC [2621]
<i>aphA3</i>	3' 5'-aminoglycoside acetyltransferase; kanamycin resistance	845	CTGGTGGGAGAAAAT GAAAACC [2636]	CCAGTTTTTCGCAATCCAC ATC [2637]
<i>blaI</i>	regulator protein	814	AGCAAGTTGAAATAT CTATGGCTGA [2574]	TCATTTAAAAATGTCICGCA ATTCTT [2575]
<i>blaR</i>	beta lactamase repressor	790	GAAAATTCACGTATGT CATGGAATC [2526]	GCATTTTTCCCAGATGGC TT [2527]
<i>blaZ</i>	beta-lactamase	827	GATAAGAGATTTGCC TATGCTTCAA [2600]	TGCTTAATTTTCCATTTCG GAT [2601]
<i>cadA</i>	Probable cadmium-transporting ATPase (Cadmium efflux ATPase)	897	TTGGATAGTTCAACAA AAACATTAAACA [2740]	CATTTTATCTTCTGTTAC CACTGGTT [2741]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>cadC</i>	Cadmium efflux system accessory protein homolog	908	TAGCAACCTCCCTTTC ATAC [2762]	ACAAAAGATATGTGTGAA GTTACC [2763]
<i>cat</i>	chloramphenicol acetyltransferase	862	CCTTCTTTGATTATG CAATTATGG [2670]	GAAGCATGGTAACCATCA CATACA [2671]
<i>dfrA</i>	S1 dihydrofolate reductase, trimethoprim resistance	859	ATGACATTATCAATAA TTGTCGCTCA [2664]	AACATGACCAGATAACTC TTTAATTTTCAT [2665]
<i>ermA</i>	rRNA methylase	852	TAGCTATCTTATCGTT GAGAAGGGAT [2650]	AAAGAAAATTGTTCCCTTCG ATAGTTTATT [2651]
<i>ermB</i>	adenine methylase	851	AACCGATACCGTTTAC GAAATTG [2648]	CGCTTGTAGAAATCCTTCT TCAACA [2649]
<i>ermC</i>	adenine methylase	846	AACACAGTCAAAACTT TATTACTTCAAAAC [2638]	TTGCATAATTATGGTCTA TTTCAATG [2639]
<i>femA</i>	factor essential for methicillin resistance	801	TAGGATTTGAACATAC TGGATTCCA [2548]	AAAGGCACTAACACACGG TCTTT [2549]
<i>femD</i>	putative factor essential for methicillin resistance	16	TCAGGTGAAATGTTA GAATCAGCA [978]	TAAGTCACCAAAATAAGAA TGGCG [979]
<i>fmhA</i>	similar to Staphylococcus aureus FemA and FemB proteins	825	GTTAACGATTGATGA AACGCAAA [2596]	TGCACCATCTTGTTCAAAT TGTT [2597]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>fthB</i>	essential for addition of glycine 1 to peptidoglycan precursor	818	GAGTTATTAAATAGTT TTGAACGCCG [2582]	TTCAGGATGTTCCCTTTTCT AAAGCT [2583]
<i>linA</i>	lincosaminide nucleotidyltransferase	850	GATATAGGATACAAA ATAGAAGTTGATTGG [2646]	GGTCTTTTCTGTAAATTC ATAACCG [2647]
<i>mecA</i>	penicillin binding protein 2'	802	ATATGAGATAGGCAT CGTTCCAAA [2550]	CTAATAGATGTGAAGTCG CTTTTCCT [2551]
<i>mecI</i>	mecI protein	812	TAATAAAACGTATGAA ATATCATCTGCA [2570]	TTTCATCTTGTGATAGATC TTCTTTTTC [2571]
<i>mecR</i>	mecI protein	798	TTTAAAGAATGGAAC CAAGATCAAA [2542]	TCGCCTTTTAAATGTGTA GCAA [2543]
<i>mreA</i>	ABC transporter	907	GCAGTATTAGTACTTG ATGAACCAACG [2760]	GACAAAACGTACAGGATG TCCATAA [2761]
<i>mreB</i>	ABC transporter	36	ATGAGGTACTCTTTAA TTAGTGGTATCTTGA [1018]	ATCAGCTAATGAAATGAA GATTGCA [1019]
<i>mreR</i>	ABC transporter	37	GAAAATACAGAACTT GATGGTGAAATG [1020]	GCAAGACTCACATACACC ATAAACTTC [1021]
<i>msrA</i>	methionine sulfoxide reductase	854	TCATAAGCTGACAGA TTTTCGATCC [2654]	CTTTTAGATGAACCTACA AATCACTTGG [2655]

(continued)

Gene symbol	Functions	gene probe SEQ ID NO	Primer forward [SEQ ID NO]	Primer reverse [SEQ ID NO]
<i>norA</i>	quinolone resistance protein	904	TTAGCTTTCAT ⁻ AATGT ⁻ CAGTTGTATTGA [2754]	ACAGTGTTC ⁻ AAATGCCG ATAAA [2755]
<i>pbpF</i>	penicillin-binding protein Pbp2b	42	AACACAATCGGAAAT GTTGGATAC [1030]	CTATCCCAATCCATAGAC GTGTTAA [1031]
<i>qacA</i>	quaternary ammonium compound resistance protein	885	CAATGGTTACAGGTT GTGGAAGA [2716]	GCCCACTACAGATTCTTC AGCTAC [2717]
<i>spc</i>	adenyltransferase AAD9	844	ATATCAGGAAAAGATT GGAAATACGG [2634]	AAAGAGGTATAGCCCCATT CTGCA [2635]

[0126] In order to obtain a high specificity level, each selected gene was compared to all other gene sequences available in the NCBI database using the BLAST algorithm. From that comparison, regions (ranging from 104 to 1434 bp) devoid of apparent homology with genes of other bacterial species and *Homo sapiens* were defined and amplified by PCR using specifically designed primers (see Tab. 6). A mixture of the total DNA from three different *S. aureus* reference strains and 100 clinical isolates was used as template for amplification of *S. aureus* gene segments, increasing therefore the chances to amplify more seldom occurring virulence and antibiotic resistance genes. PCR products were cloned into the plasmid pCR 2.1 -Topo Vector (Invitrogen, Karlsruhe, Germany) which were used to transform competent *Escherichia coli* (XL-1-Blue) cells using the Calcium Chloride protocol (Seidman, C.E. et al., in: Ausubel, F.M. (ed.), Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (2000)). Recombinant plasmids containing selected gene segments were screened by restriction analysis and verified by sequencing. The plasmid library constructed was used for re-amplification and production of the bulk DNA (10 µg at a concentration of 1 µM) from each clone necessary for printing the microchips. A Microgrid II spotter (BioRobotics, Cambridge, UK) and CMT-GAPS™ coated glass slides (Corning Incorporated, Corning, USA) were used. The complete array of 140 segments of genes was spotted in 3 replicates per slide.

C) DNA purification

a) Sample preparation

[0127] Bacterial cultures: Overnight cultures (5 ml) were harvested at 2,560g for 10 minutes. After discarding the supernatant the pellet was washed in 1 ml TE (10 mM Tris-HCl, pH 7.5 - 1 mM EDTA) and recovered by centrifugation at 17,900 g for 2 min.

[0128] Blood cultures: One ml of blood culture was mixed with 1 ml 0.1% Triton®-X-100 and kept at room temperature for 5 min in order to disrupt blood human cells and resolve bacterial clumps. Bacterial cells were then harvested at 17,900 g for 10 min. Pellets were washed in 1 ml TE and recovered as described above.

b) Purification of DNA

[0129] Pellets of harvested cells were resuspended in 500 µl lysis buffer (20 mM Tris-HCl, pH 8.0 - 2 mM EDTA, pH 8.0 - 1.2% Triton®-X-100). To promote bacterial lysis, lysozyme and lysostaphin (Sigma, Taufkirchen, Germany) were added to reach a final concentration of 0.8 mg/ml and 0.2 mg/ml respectively. To lyse Gram negative bacterial cells, only lysozyme in the indicated concentration was used. Samples were then incubated for one hour at 37°C. After treatment with Proteinase K (1 mg/ml) (Sigma, Taufkirchen, Germany) for 5 hours at 55 °C under mild agitation, the samples were heated at 65°C for 30 min to inactivate Proteinase K and then cooled down to 37°C. Finally, a RNase A treatment (0.2 mg/ml) was carried out for 1 hour at 37°C. A pretreatment with CTAB (Cethyltrimethylammonium bromide) was performed in order to release DNA from polysaccharide DNA complexes (Murray, M.G. and Thopson, W.F., Nucl. Acid Res. 8: 4321-4325 (1980)). Salt concentration was adjusted to 0.7 M by adding 5 M NaCl. After thoroughly mixing, a 10% CTAB-0.7M NaCl solution was added to adjust the CTAB concentration to 1%.

[0130] The mixture was subsequently incubated under rotation for 20 min at 65°C and then extracted with one volume of chloroform/isoamyl alcohol (24:1). The samples were spun in a microcentrifuge (17,900 g) at room temperature. The aqueous phase was extracted once with chloroform/isoamyl alcohol (24:1), once with phenol/chloroform/isoamyl alcohol (25:24:1) and finally with chloroform/ isoamyl alcohol (25:24:1). Genomic DNA in the aqueous phase was sonified (3 x 10 s at 12% amplitude with 20 s breaks between pulses) in a Digital Sonifier (Branson, Schwaebisch Gmuend, Germany) to obtain fragments of around 1 kb, then precipitated with one volume of isopropanol and pelleted by centrifugation for 30 min at 4°C in a microcentrifuge at 17,900 g. The pellets were washed in 70% ethanol and resuspended in 50-100 µl TE (10 mM Tris-HCl, pH 7.5 - 1 mM EDTA). This DNA preparation was used when a high yield (hundreds of µg) was necessary, for example to prepare samples for several hybridisations experiments.

[0131] A second protocol using DNeasy Tissue Kit (QIAGEN, Hilden, Germany) adapted to bacterial cells and allowing DNA preparation in two hours, was also used when fast preparation was the priority. The abbreviations below pertain to the manufacturer's abbreviations for buffers used in the kit. The bacterial pellet was resuspended in 1 ml ddH₂O and the cell suspension frozen in liquid N₂ for 1 minute and then placed in a 60°C thermo-block for 2 minutes. Such a treatment was repeated once and bacteria were centrifuged again for 5 minutes at 14,000g. The resulting pellet was resuspended in 180 µl lysis buffer (20 mM Tris-HCl, pH 8.0 - 2 mM EDTA, pH 8.0 - 1.2% Triton-X-100). Specifically for *S. aureus* DNA preparation, lysostaphin (0.2mg/ml) was added and incubated 1 hour at 37°C. After, 200 µl of buffer AL (for gram positive bacteria) or buffer ATL (for gram negative) and 25 µl of the Proteinase K solution delivered with the kit were added and incubated at 70°C for 30 minutes. 200 µl of 100% ethanol were added and the suspension transferred to a DNeasy Mini Column placed into a collection tube. The column was centrifuged at 6,000 g for 1 minute, washed first with 500 µl of buffer AW1, centrifuged at 6,000 g for 1 minute, washed then with 500 µl of buffer AW2, and centrifuged

at 14,000 g for 3 minutes. The column was then placed in a 1.5 ml tube and centrifuged once more at 14,000 g for 1 minute. DNA was eluted with 130 μ l of buffer AE. After one minute the column was centrifuged at 6,000g for 1 minute. The eluate was re-loaded in the column and centrifuged again under the same conditions in order to increase the DNA yield.

D) DNA labelling

[0132] Different amounts of DNA (5 ng to 5 μ g) were labelled with 3 μ l either of Cy5-dCTP or Cy3-dCTP (Amersham Pharmacia Biotech Europe, Freiburg, Germany) by random priming (1 x random primer/Klenow reaction buffer) using Klenow Polymerase (50units) (both from BioPrime DNA labelling Kit, Invitrogen, Karlsruhe, Germany) in the presence of 0.12 mM dATP's, dGTP's and dTTP's and 0.06 mM dCTP's, in a total volume of 50 μ l. After 2 hours incubation at 37°C, the reaction was interrupted by adding 5 μ l of 0.5 M EDTA and the probe purified either by MiniElute PCR or QIAquick Purification Kits (QIAGEN, Hilden, Germany), depending on the amount of labelled DNA applying two wash and two elution steps.

E) Hybridisation and detection procedure

[0133] All experiments described in the present example represent co-hybridisation of two different DNA samples labelled respectively with Cy3 and Cy5. Cy3 and Cy5 belong to the cyanine family of fluorophores and were used as reporter molecules. The photochemical properties of the two CyDye fluors were as follows: Absorption maximum at 550 nm and emission maximum at 570 nm for Cy3 and for Cy5 at 649 nm and 670 nm, respectively.

[0134] After purification, Cy3 and Cy5 labelled DNA were pooled and 10 μ g of Salmon Sperm DNA and 50 μ g of polyA DNA were added. The mixture was frozen in liquid nitrogen and lyophilized in the dark. DNA microchips were automatically hybridised in a GeneTac Hybridisation Station (Genomic Solutions, Harvard, USA) following the Corning protocol.

[0135] Shortly, 110 μ l of pre-hybridisation buffer (25% Formamide, 5x SSC, 0.1% SDS, 10 mg/ml BSA) were added to each slide and incubated for one hour at 42°C. Lyophilized samples were resuspended in 110 μ l of hybridisation buffer (25% Formamide, 5x SSC, 0.1% SDS), denatured for 3 minutes at 90°C, added to the slides, and incubated 4 hours at 42°C. After several washing steps using successively 2 x SSC/0.1 % SDS, 0.1 x SSC/0.1 % SDS, and 0.1 x SSC, slides were dried by a 2 min centrifugation step (1000 g) and read in a Scan Array 5000 (Perkin Elmer, Boston, USA) using emission filters for Cy3 and Cy5 in two separate channels. Fluorescence intensities as hybridisation indicators were then analyzed by the software ImaGene (BioDiscovery, Marina Del Rey, USA). Spots were found and segmented in order to select areas of recognizable signals for analysis. Intensity of fluorescence of each spot was measured, signal to local background ratios were calculated, spot morphology and deviation from expected spot position were considered. Cut off values for those parameters were empirically determined in pilot experiments and used to tag spots either as positive or as negative.

F) Validation of the detection system

[0136] The experimental approach adopted in present example required dual-dye hybridisations. It was therefore necessary to verify at first whether DNA samples from the same source, labelled with one or the other fluorochrome, would produce the same hybridisation pattern. Co-hybridisation experiments, combining two identical samples of 2 μ g of *S. aureus* DNA, produced strictly similar hybridisation results whatever fluorochrome was used for labelling (Fig. 2A). For better presentation gray scale images from scanning were converted in false-color, where green and red color represent intensity of Cy3 and Cy5 fluorochromes respectively. All spots showed double-hybridisation - yellow color meaning the overlay between green (here assigned to Cy3 labelled DNA) and red signals (Cy5 labelled DNA). Signal intensities from both channels strongly correlated ($r^2=0,97$) (Fig. 2B).

G) Sensitivity of detection

[0137] *S. aureus* DNA samples in decreasing amounts (from 2 μ g to 5 ng) were labelled and hybridised in order to determine the minimum amount of DNA producing the expected hybridisation pattern for a certain strain. Such expected patterns were defined as those produced by the hybridisation of 2 μ g of DNA. From 2 μ g to 50 ng no significant differences in the hybridisation pattern were observed with no false negative spots. Detection of 20 ng DNA was still satisfying with only 5% of false negative and false positive. However, 5 ng of labelled DNA yielded weak signals with almost 95% of false negative spots (data not shown). The limit of sensitivity of the *S. aureus* microarray was then considered as being 20 ng DNA which corresponds approximately to 7×10^6 *S. aureus* CFU (*S. aureus* genome 2.5×10^6 bp. 2.8 fg DNA per cell).

H) Specificity of detection

[0138] The specificity of the *S. aureus* microchip was demonstrated by six independently performed co-hybridisation experiments. Visual examination of pictures showing results of co-hybridisation of *S. aureus* DNA with *Pseudomonas aeruginosa* or *Escherichia coli* DNA revealed no cross-hybridisation between *S. aureus* selected gene segments and DNA probes from those Gram negative bacteria (data not shown). Transcribing these data in a bar code showing positive or negative spots (Fig. 3A and B) confirmed that only the *S. aureus* DNA sample hybridised with spotted probes.

[0139] The specificity of the microarray could be demonstrated even below the genus level. As shown in Fig. 4, some spotted *S. aureus* probes cross-hybridised with *S. epidermidis* and *S. saprophyticus* DNA samples. This is not surprising as these species are phylogenetically closely related. However, genes coding for *S. aureus* specific proteins as nuclease (*nuc*), clumping factors A and B (*clfA* and *B*), protein A (*spa*), V8 serine protease (*sprV8*) and alpha and beta hemolysins (*hla* and *hly*) exclusively hybridised with *S. aureus* DNA. The presence/absence of such genes allowed unambiguous discrimination between *S. aureus* and CoNS.

I) *S. aureus* strain profiling

[0140] The principle of the *S. aureus* microarray was tested as a tool for strain profiling. A distinctive hybridisation pattern could be established for reference strains and 10 selected clinical isolates. For instance when DNA from clinical isolates T100 and T103 were labelled with Cy5 and Cy3, respectively, and co-hybridised, both isolates were identified as *S. aureus*, since both contained species-specific genes as e.g. clumping factor A and B (Fig. 5A).

[0141] Moreover, both strains are methicillin resistant (*mecA* positive), but only T100 contained the beta-lactamase gene. The hybridisation of T103 DNA reveals the presence of *ermA*, *ermB* and *aacA* genes indicating that the strain is resistant to erythromycin and aminoglycosides.

[0142] Apparently, T103 harbors the genes encoding enterotoxins A (*eta*) and B (*etb*) while in T100 the gene encoding enterotoxin C (*etc*) is present. The presence or absence of these genes was confirmed by PCR assays (Fig. 5B) and the antibiotic resistance was verified by classical antibiograms (Sahm, D. & Washington, J. A. (1991). Antibacterial susceptibility tests: dilution methods. In: Manual of Clinical Microbiology (Balows, A., Ed.), pp. 1105-16. American Society for Microbiology, Washington DC, USA) (data not shown).

J) Detection of *S. aureus* in spiked positive BACTEC® cultures

[0143] One possible application of the *S. aureus* microarray is to detect the bacterium growing in blood culture, i.e. after the BACTEC® signals bacterial growth. Blood culture bottles were spiked with 100 CFU of *S. aureus*. After the automated culturing system indicated bacterial growth, 1 ml was withdrawn for DNA extraction.

[0144] As shown in Fig. 6A, DNA samples prepared from sterile blood culture show no crosshybridisation with spotted *S. aureus* probes. A 2 µg DNA sample derived from blood culture containing *S. aureus* cells revealed a hybridisation pattern almost completely identical to a DNA sample isolated from an overnight LB culture inoculated with a *S. aureus* colony (Fig. 6B).

[0145] These data underscore the high sensitivity and specificity of the detection system since blood culture DNA comprises a mixture of human and bacterial DNA. Co-hybridisation between DNA from blood culture positive for *S. aureus* and CoNS DNA also allowed clear identification since only the *S. aureus* probe hybridised to *S. aureus* species-specific genes (data not shown).

K) Detection of *S. aureus* in positive BACTEC® cultures inoculated with clinical specimens

[0146] Co-hybridisation with DNA from clinical blood cultures positive for *S. aureus* and CoNS (*Staphylococcus epidermidis*), *Streptococcus mitis*, *E. coli* and *Klebsiella oxytoca* allowed clear species identification since the *S. aureus* probes hybridised to *S. aureus* species-specific genes only. *Staphylococcus epidermidis* positive blood culture DNA hybridised to staphylococcal metabolic genes and to some antibiotic resistance determinant genes only. No cross-hybridisation was detected between DNA from the two gram-negative strains and the *Streptococcus* strain and *S. aureus* spotted gene probes (data not shown).

Sequence Listing - Free text

[0147] a) Probe sequences

EP 1 770 171 A1

SEQ ID NO	Probe name	Template source
1	cataSaur_1_1	<i>Staphylococcus aureus</i>
2	cataSaur_1_2	<i>Staphylococcus aureus</i>
3	clfA_1_1	<i>Staphylococcus aureus</i>
4	clfB_1_1	<i>Staphylococcus aureus</i>
5	coa_1_1	<i>Staphylococcus aureus</i>
6	coa_1_2	<i>Staphylococcus aureus</i>
7	l-clpC_1_1	<i>Staphylococcus aureus</i>
8	l-clpP_1_1	<i>Staphylococcus aureus</i>
9	l-ctaA_1_1	<i>Staphylococcus aureus</i>
10	l-ctsR_1_1	<i>Staphylococcus aureus</i>
11	l-dltA_1_1	<i>Staphylococcus aureus</i>
12	l-dltB_1_1	<i>Staphylococcus aureus</i>
13	l-dltC_1_1	<i>Staphylococcus aureus</i>
14	l-dnaK_1_1	<i>Staphylococcus aureus</i>
15	l-elkT_1_1	<i>Staphylococcus aureus</i>
16	l-femD_1_1	<i>Staphylococcus aureus</i>
17	l-glnA_1_1	<i>Staphylococcus aureus</i>
18	l-glnR_1_1	<i>Staphylococcus aureus</i>
19	l-grlA_1_1	<i>Staphylococcus aureus</i>
20	l-grlB_1_1	<i>Staphylococcus aureus</i>
21	l-groEL_1_1	<i>Staphylococcus aureus</i>
22	l-groES_1_1	<i>Staphylococcus aureus</i>
23	l-hemA_1_1	<i>Staphylococcus aureus</i>
24	l-hemE_1_1	<i>Staphylococcus aureus</i>
25	l-hemH_1_1	<i>Staphylococcus aureus</i>
26	l-hemL_1_1	<i>Staphylococcus aureus</i>
27	l-hemY_1_1	<i>Staphylococcus aureus</i>
28	l-lepA_1_1	<i>Staphylococcus aureus</i>
29	l-lrgA_1_1	<i>Staphylococcus aureus</i>
30	l-lrgB_1_1	<i>Staphylococcus aureus</i>
31	l-lytM_1_1	<i>Staphylococcus aureus</i>
32	l-menB_1_1	<i>Staphylococcus aureus</i>
33	l-menD_1_1	<i>Staphylococcus aureus</i>
34	l-menE_1_1	<i>Staphylococcus aureus</i>
35	l-menF_1_1	<i>Staphylococcus aureus</i>
36	l-mreB_1_1	<i>Staphylococcus aureus</i>
37	l-mreR_1_1	<i>Staphylococcus aureus</i>
38	l-mutL_1_1	<i>Staphylococcus aureus</i>
39	l-mutS_1_1	<i>Staphylococcus aureus</i>

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SEQ ID NO	Probe name	Template source
40	I-NAG_1_1	<i>Staphylococcus aureus</i>
41	I-pbg_1_1	<i>Staphylococcus aureus</i>
42	I-pbpF_1_1	<i>Staphylococcus aureus</i>
43	I-pdhB_1_1	<i>Staphylococcus aureus</i>
44	I-pdhC_1_1	<i>Staphylococcus aureus</i>
45	I-rsbU_1_1	<i>Staphylococcus aureus</i>
46	I-rsbV_1_1	<i>Staphylococcus aureus</i>
47	I-rsbW_1_1	<i>Staphylococcus aureus</i>
48	I-sgp_1_1	<i>Staphylococcus aureus</i>
49	I-sirR_1_1	<i>Staphylococcus aureus</i>
50	I-sodA_1_1	<i>Staphylococcus aureus</i>
51	I-sodB_1_1	<i>Staphylococcus aureus</i>
52	I-sstA_1_1	<i>Staphylococcus aureus</i>
53	I-sstB_1_1	<i>Staphylococcus aureus</i>
54	I-sstC_1_1	<i>Staphylococcus aureus</i>
55	I-sstD_1_1	<i>Staphylococcus aureus</i>
56	I-trx_1_1	<i>Staphylococcus aureus</i>
57	I-yhiN_1_1	<i>Staphylococcus aureus</i>
58	epiP-bsaP_1_1	<i>Staphylococcus aureus</i>
59	geh_1_1	<i>Staphylococcus aureus</i>
60	gyrA_1_1	<i>Staphylococcus aureus</i>
61	gyrB_1_1	<i>Staphylococcus aureus</i>
62	hemB_1_1	<i>Staphylococcus aureus</i>
63	hemC_1_1	<i>Staphylococcus aureus</i>
64	hemD_1_1	<i>Staphylococcus aureus</i>
65	hemN_1_1	<i>Staphylococcus aureus</i>
66	hsdS_1_1	<i>Staphylococcus aureus</i>
67	hsdS_2_1	<i>Staphylococcus aureus</i>
68	lip_1_1	<i>Staphylococcus aureus</i>
69	menC_1_1	<i>Staphylococcus aureus</i>
70	murC_1_1	<i>Staphylococcus aureus</i>
71	nuc_1_1	<i>Staphylococcus aureus</i>
72	pdhD_1_1	<i>Staphylococcus aureus</i>
73	rpoB_1_1	<i>Staphylococcus aureus</i>
74	SAV0431_1_1	<i>Staphylococcus aureus</i>
75	SAV0439_1_1	<i>Staphylococcus aureus</i>
76	SAV0440_1_1	<i>Staphylococcus aureus</i>
77	SAV0441_1_1	<i>Staphylococcus aureus</i>

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SEQ ID NO	Probe name	Template source
78	sigB_1_1	<i>Staphylococcus aureus</i>
79	spa_1_2	<i>Staphylococcus aureus</i>
80	sstC_1_1	<i>Staphylococcus aureus</i>
81	tag_1_1	<i>Staphylococcus aureus</i>
82	tyrA_1_1	<i>Staphylococcus aureus</i>
83	l-aroC_1_1	<i>Staphylococcus aureus</i>
84	l-aroA_1_1	<i>Staphylococcus aureus</i>
85	l-cna_1_1	<i>Staphylococcus aureus</i>
86	l-ebpS_1_1	<i>Staphylococcus aureus</i>
87	l-eno_1_1	<i>Staphylococcus aureus</i>
88	l-fbpA_1_1	<i>Staphylococcus aureus</i>
89	l-fib_1_1	<i>Staphylococcus aureus</i>
90	l-fnbB_1_1	<i>Staphylococcus aureus</i>
91	l-srtA_1_1	<i>Staphylococcus aureus</i>
92	l-stpC_1_1	<i>Staphylococcus aureus</i>
93	l-fnbA_1_1	<i>Staphylococcus aureus</i>
94	l-spa_1_1	<i>Staphylococcus aureus</i>
95	l-aroE_1_1	<i>Staphylococcus aureus</i>
96	l-aroF_1_1	<i>Staphylococcus aureus</i>
97	l-aroG_1_1	<i>Staphylococcus aureus</i>
98	l-asp23_1_1	<i>Staphylococcus aureus</i>
99	l-atl_1_1	<i>Staphylococcus aureus</i>
100	bsaE_1_1	<i>Staphylococcus aureus</i>
101	bsaG_1_1	<i>Staphylococcus aureus</i>
102	cap5h_1_1	<i>Staphylococcus aureus</i>
103	cap5i_1_1	<i>Staphylococcus aureus</i>
104	cap5j_1_1	<i>Staphylococcus aureus</i>
105	cap5k_1_1	<i>Staphylococcus aureus</i>
106	cap8H_1_1	<i>Staphylococcus aureus</i>
107	cap8I_1_1	<i>Staphylococcus aureus</i>
108	cap8J_1_1	<i>Staphylococcus aureus</i>
109	cap8K_1_1	<i>Staphylococcus aureus</i>
110	l-hld_1_1	<i>Staphylococcus aureus</i>
111	l-hysA_1_1	<i>Staphylococcus aureus</i>
112	l-IgGbg_1_1	<i>Staphylococcus aureus</i>
113	EDIN_1_1	<i>Staphylococcus aureus</i>
114	eta_1_1	<i>Staphylococcus aureus</i>
115	etb_1_1	<i>Staphylococcus aureus</i>

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SEQ ID NO	Probe name	Template source
116	hglA_1_1	<i>Staphylococcus aureus</i>
117	hglA_2_1	<i>Staphylococcus aureus</i>
118	hglB_1_1	<i>Staphylococcus aureus</i>
119	hglC_2_1	<i>Staphylococcus aureus</i>
120	hla_1_1	<i>Staphylococcus aureus</i>
121	hlb_1_2	<i>Staphylococcus aureus</i>
122	lukF_1_1	<i>Staphylococcus aureus</i>
123	lukS_1_1	<i>Staphylococcus aureus</i>
124	lukS_2_1	<i>Staphylococcus aureus</i>
125	NAG_1_1	<i>Staphylococcus aureus</i>
126	sak_1_1	<i>Staphylococcus aureus</i>
127	sea_1_1	<i>Staphylococcus aureus</i>
128	seb_1_1	<i>Staphylococcus aureus</i>
129	sec1_1_1	<i>Staphylococcus aureus</i>
130	seg_1_1	<i>Staphylococcus aureus</i>
131	seh_1_1	<i>Staphylococcus aureus</i>
132	sel_1_1	<i>Staphylococcus aureus</i>
133	set 15_1_1	<i>Staphylococcus aureus</i>
134	set6_1_1	<i>Staphylococcus aureus</i>
135	set7_1_1	<i>Staphylococcus aureus</i>
136	set8_1_1	<i>Staphylococcus aureus</i>
137	sprV8_1_1	<i>Staphylococcus aureus</i>
138	tst_1_1	<i>Staphylococcus aureus</i>
139	l-sdrC_1_1	<i>Staphylococcus aureus</i>
140	l-sdrD_1_1	<i>Staphylococcus aureus</i>
141	l-sdrE_1_1	<i>Staphylococcus aureus</i>
142	b1169_1_1	<i>Escherichia coli</i>
143	envZ_1_1	<i>Escherichia coli</i>
144	fliCb_1_1	<i>Escherichia coli</i>
145	nfrB_1_1	<i>Escherichia coli</i>
146	nlpA_1_1	<i>Escherichia coli</i>
147	pilAe_1_1	<i>Escherichia coli</i>
148	yacH_1_1	<i>Escherichia coli</i>
149	yagX_1_1	<i>Escherichia coli</i>
150	ycdS_1_1	<i>Escherichia coli</i>
151	yciQ_1_1	<i>Escherichia coli</i>
152	ym cA_1_1	<i>Escherichia coli</i>
153	b1202_1_1	<i>Escherichia coli</i>

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SEQ ID NO	Probe name	Template source
154	eae_1_1	<i>Escherichia coli</i>
155	eltB_1_1	<i>Escherichia coli</i>
156	escR_1_1	<i>Escherichia coli</i>
157	escT_1_1	<i>Escherichia coli</i>
158	escU_1_1	<i>Escherichia coli</i>
159	espB_1_1	<i>Escherichia coli</i>
160	fes_1_1	<i>Escherichia coli</i>
161	fes_2_1	<i>Escherichia coli</i>
162	fteA_1_1	<i>Escherichia coli</i>
163	hlyA_1_1	<i>Escherichia coli</i>
164	hlyB_1_1	<i>Escherichia coli</i>
165	iucA_1_1	<i>Escherichia coli</i>
166	iucB_1_1	<i>Escherichia coli</i>
167	iucC_1_1	<i>Escherichia coli</i>
168	papG_1_1	<i>Escherichia coli</i>
169	rfbE_1_1	<i>Escherichia coli</i>
170	shuA_1_1	<i>Escherichia coli</i>
171	SLTII_1_1	<i>Escherichia coli</i>
172	toxA- LTPA_1_1	<i>Escherichia coli</i>
173	VT2vaB_1_1	<i>Escherichia coli</i>
174	ardeSE0106_1_1	<i>Staphylococcus epidermidis</i>
175	ardeSE0107_1_1	<i>Staphylococcus epidermidis</i>
176	aroISE0105_1_1	<i>Staphylococcus epidermidis</i>
177	atlE_1_1	<i>Staphylococcus epidermidis</i>
178	agrB_1_1	<i>Staphylococcus epidermidis</i>
179	agrC_1_1	<i>Staphylococcus epidermidis</i>
180	alphSE1368_1_1	<i>Staphylococcus epidermidis</i>
181	gad_1_1	<i>Staphylococcus epidermidis</i>
182	glucSE1191_1_1	<i>Staphylococcus epidermidis</i>
183	hsp10_1_1	<i>Staphylococcus epidermidis</i>
184	icaA_1_1	<i>Staphylococcus epidermidis</i>
185	icaB_1_1	<i>Staphylococcus epidermidis</i>
186	mvaSSepid_1_1	<i>Staphylococcus epidermidis</i>
187	nitreSE1972_1_1	<i>Staphylococcus epidermidis</i>
188	nitreSE1974_1_1	<i>Staphylococcus epidermidis</i>
189	nitreSE1975_1_1	<i>Staphylococcus epidermidis</i>
190	oiamtSE1209_1_1	<i>Staphylococcus epidermidis</i>
191	ORF1Sepid_1_1	<i>Staphylococcus epidermidis</i>

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SEQ ID NO	Probe name	Template source
192	ORF3bSepid_1_1	<i>Staphylococcus epidermidis</i>
193	qacR_1_1	<i>Staphylococcus epidermidis</i>
194	sin_1_1	<i>Staphylococcus epidermidis</i>
195	ureSE1861_1_1	<i>Staphylococcus epidermidis</i>
196	ureSE1863_1_1	<i>Staphylococcus epidermidis</i>
197	ureSE1864_1_1	<i>Staphylococcus epidermidis</i>
198	ureSE1865_1_1	<i>Staphylococcus epidermidis</i>
199	ureSE1867_1_1	<i>Staphylococcus epidermidis</i>
200	gcaD_1_1	<i>Staphylococcus epidermidis</i>
201	hld_orf5_1_1	<i>Staphylococcus epidermidis</i>
202	icaC_1_1	<i>Staphylococcus epidermidis</i>
203	icaD_1_1	<i>Staphylococcus epidermidis</i>
204	icaR_1_1	<i>Staphylococcus epidermidis</i>
205	psm_betaiand2_1_1	<i>Staphylococcus epidermidis</i>
206	purR_1_1	<i>Staphylococcus epidermidis</i>
207	spoVG_1_1	<i>Staphylococcus epidermidis</i>
208	yabJ_1_1	<i>Staphylococcus epidermidis</i>
209	folQShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
210	mvaCShaemolyticus_1_1	<i>Staphylococcus haemolyticus</i>
211	mvaDShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
212	mvaK1Shaemolyticus_1_1	<i>Staphylococcus haemolyticus</i>
213	mvaSShaemolyticus_1_1	<i>Staphylococcus haemolyticus</i>
214	RNApolsigm_1_1	<i>Staphylococcus haemolyticus</i>
215	lipShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
216	agrB2Stalugd_1_1	<i>Staphylococcus lugdunensis</i>
217	agrC2Stalugd_1_1	<i>Staphylococcus lugdunensis</i>
218	agrCStalugd_1_1	<i>Staphylococcus lugdunensis</i>
219	slamStalugd_1_1	<i>Staphylococcus lugdunensis</i>
220	fblStalugd_1_1	<i>Staphylococcus lugdunensis</i>
221	slushABCStalugd_1_1	<i>Staphylococcus lugdunensis</i>
222	RNApolsigmSsapro_1_1	<i>Staphylococcus saprophyticus</i>
223	RNApolsigmSsapro_1_2	<i>Staphylococcus saprophyticus</i>
224	msrw1Stwar_1_1	<i>Staphylococcus warneri</i>
225	nukMStwar_1_1	<i>Staphylococcus warneri</i>
226	proDStwar_1_1	<i>Staphylococcus warneri</i>
227	proMStwar_1_1	<i>Staphylococcus warneri</i>
228	sigrpoStwar_1_1	<i>Staphylococcus warneri</i>
229	tnpStwar_1_1	<i>Staphylococcus warneri</i>

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SEQ ID NO	Probe name	Template source
230	gehASTwar_1_1	<i>Staphylococcus warneri</i>
231	ARG56_1_1	<i>Candida albicans</i>
232	ASL43f_1_1	<i>Candida albicans</i>
233	BGL2_1_1	<i>Candida albicans</i>
234	CACHS3_1_1	<i>Candida albicans</i>
235	CCT8_1_1	<i>Candida albicans</i>
236	CDC37_1_1	<i>Candida albicans</i>
237	CEF3_1_1	<i>Candida albicans</i>
238	CHS1_1_1	<i>Candida albicans</i>
239	CHS2_1_1	<i>Candida albicans</i>
240	CHS4_1_1	<i>Candida albicans</i>
241	CHS5_1_1	<i>Candida albicans</i>
242	CHT1_1_1	<i>Candida albicans</i>
243	CHT2_1_1	<i>Candida albicans</i>
244	CHT4_1_1	<i>Candida albicans</i>
245	CSA1_1_1 1	<i>Candida albicans</i>
246	5triphosphatase_1_1	<i>Candida albicans</i>
247	AAF1_1_1 1	<i>Candida albicans</i>
248	ADH1_1_1	<i>Candida albicans</i>
249	ALS1_1_1	<i>Candida albicans</i>
250	ALS7_1_1	<i>Candida albicans</i>
251	EDT1_1_1	<i>Candida albicans</i>
252	ELF_1_1	<i>Candida albicans</i>
253	ESS1_1_1	<i>Candida albicans</i>
254	FAL1_1_1	<i>Candida albicans</i>
255	GAP1_1_1	<i>Candida albicans</i>
256	GNA1_1_1	<i>Candida albicans</i>
257	GSC1_1_1	<i>Candida albicans</i>
258	GSL1_1_1	<i>Candida albicans</i>
259	HIS1_1_1	<i>Candida albicans</i>
260	HTS1_1_1	<i>Candida albicans</i>
261	HWP1_2_1	<i>Candida albicans</i>
262	HYR1_1_1	<i>Candida albicans</i>
263	NT1a_1_1	<i>Candida albicans</i>
264	KRE15f_1_1	<i>Candida albicans</i>
265	KRE6_1_1	<i>Candida albicans</i>
266	KRE9_1_1	<i>Candida albicans</i>
267	MIG1_1_1	<i>Candida albicans</i>

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SEQ ID NO	Probe name	Template source
268	MLS1_1_1	<i>Candida albicans</i>
269	MP65_1_1	<i>Candida albicans</i>
270	NDE1_1_1	<i>Candida albicans</i>
271	PFK2_1_1	<i>Candida albicans</i>
272	PHR1_1_1	<i>Candida albicans</i>
273	PHR2_1_1	<i>Candida albicans</i>
274	PHR3_1_1	<i>Candida albicans</i>
275	PRA1_1_1	<i>Candida albicans</i>
276	PRS1_1_1	<i>Candida albicans</i>
277	RBT1_1_1	<i>Candida albicans</i>
278	RBT4_1_1	<i>Candida albicans</i>
279	RHO1_1_1	<i>Candida albicans</i>
280	RNR1_1_1	<i>Candida albicans</i>
281	RPB7_1_1	<i>Candida albicans</i>
282	RPL13_1_1	<i>Candida albicans</i>
283	RVS167_1_1	<i>Candida albicans</i>
284	SHA3_1_1	<i>Candida albicans</i>
285	SKN1_1_1	<i>Candida albicans</i>
286	SRB1_1_1	<i>Candida albicans</i>
287	TCA1_1_1	<i>Candida albicans</i>
288	TRP1_1_1	<i>Candida albicans</i>
289	YAE1_1_1	<i>Candida albicans</i>
290	YRB1_1_1	<i>Candida albicans</i>
291	YST1exon2_1_1	<i>Candida albicans</i>
292	CCN1_1_1	<i>Candida albicans</i>
293	CDC28_1_1	<i>Candida albicans</i>
294	CLN2_1_1	<i>Candida albicans</i>
295	CPH1_1_1	<i>Candida albicans</i>
296	CYB1_1_1	<i>Candida albicans</i>
297	EFG1_1_1	<i>Candida albicans</i>
298	MNT1_1_1	<i>Candida albicans</i>
299	RBF1_1_1	<i>Candida albicans</i>
300	RBF1_2_1	<i>Candida albicans</i>
301	RIM101_1_1	<i>Candida albicans</i>
302	RIM8_1_1	<i>Candida albicans</i>
303	SEC14_1_1	<i>Candida albicans</i>
304	SEC4_1_1	<i>Candida albicans</i>
305	TUP1_1_1	<i>Candida albicans</i>

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SEQ ID NO	Probe name	Template source
306	YPT1_1_1	<i>Candida albicans</i>
307	ZNF1CZF1_2_1	<i>Candida albicans</i>
308	arcA_1_1	<i>Enterococcus faecalis</i>
309	arcC_1_1	<i>Enterococcus faecalis</i>
310	bkdA_1_1	<i>Enterococcus faecalis</i>
311	cad_1_1	<i>Enterococcus faecalis</i>
312	camE1_1_1	<i>Enterococcus faecalis</i>
313	esrA_1_1	<i>Enterococcus faecalis</i>
314	dacA_1_1	<i>Enterococcus faecalis</i>
315	dfr_1_1	<i>Enterococcus faecalis</i>
316	dhoD1a_1_1	<i>Enterococcus faecalis</i>
317	ABC-eltA_1_1	<i>Enterococcus faecalis</i>
318	agrBfs_1_1	<i>Enterococcus faecalis</i>
319	agrCfs_1_1	<i>Enterococcus faecalis</i>
320	dnaE_1_1	<i>Enterococcus faecalis</i>
321	ebsA_1_1	<i>Enterococcus faecalis</i>
322	ebsB_1_1	<i>Enterococcus faecalis</i>
323	eep_1_1	<i>Enterococcus faecalis</i>
324	efaR_1_1	<i>Enterococcus faecalis</i>
325	gls24_glsB_1_1	<i>Enterococcus faecalis</i>
326	gph_1_1	<i>Enterococcus faecalis</i>
327	gyrAEf_1_1	<i>Enterococcus faecalis</i>
328	metEf_1_1	<i>Enterococcus faecalis</i>
329	mntHCb2_1_1	<i>Enterococcus faecalis</i>
330	mob2_1_1	<i>Enterococcus faecalis</i>
331	mvaD_1_1	<i>Enterococcus faecalis</i>
332	mvaE_1_1	<i>Enterococcus faecalis</i>
333	parC_1_1	<i>Enterococcus faecalis</i>
334	pcfG_1_1	<i>Enterococcus faecalis</i>
335	phoZ_1_1	<i>Enterococcus faecalis</i>
336	polC_1_1	<i>Enterococcus faecalis</i>
337	ptb_1_1	<i>Enterococcus faecalis</i>
338	reeS1_1_1	<i>Enterococcus faecalis</i>
339	rpoN_1_1	<i>Enterococcus faecalis</i>
340	tms_1_1	<i>Enterococcus faecalis</i>
341	tyrDC_1_1	<i>Enterococcus faecalis</i>
342	tyrS_1_1	<i>Enterococcus faecalis</i>
343	asa1_1_1	<i>Enterococcus faecalis</i>

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SEQ ID NO	Probe name	Template source
344	asp1_1_1	<i>Enterococcus faecalis</i>
345	cgh_1_1	<i>Enterococcus faecalis</i>
346	cylA_1_1	<i>Enterococcus faecalis</i>
347	cylB_1_1	<i>Enterococcus faecalis</i>
348	cylL_1_1	<i>Enterococcus faecalis</i>
349	cylL_cylS_1_1	<i>Enterococcus faecalis</i>
350	cylM_1_1	<i>Enterococcus faecalis</i>
351	ace_1_1	<i>Enterococcus faecalis</i>
352	ef00108_1_1	<i>Enterococcus faecalis</i>
353	ef00109_1_1	<i>Enterococcus faecalis</i>
354	ef0011_1_1	<i>Enterococcus faecalis</i>
355	ef00113_1_1	<i>Enterococcus faecalis</i>
356	ef0012_1_1	<i>Enterococcus faecalis</i>
357	ef0022_1_1	<i>Enterococcus faecalis</i>
358	ef0031_1_1	<i>Enterococcus faecalis</i>
359	ef0032_1_1	<i>Enterococcus faecalis</i>
360	ef0040_1_1	<i>Enterococcus faecalis</i>
361	ef0058_1_1	<i>Enterococcus faecalis</i>
362	enIA_1_1	<i>Enterococcus faecalis</i>
363	esa_1_1	<i>Enterococcus faecalis</i>
364	esp_1_1	<i>Enterococcus faecalis</i>
365	gelE_1_1	<i>Enterococcus faecalis</i>
366	groEL_1_1	<i>Enterococcus faecalis</i>
367	groES_1_1	<i>Enterococcus faecalis</i>
368	rt1_1_1	<i>Enterococcus faecalis</i>
369	sala_1_1	<i>Enterococcus faecalis</i>
370	salb_1_1	<i>Enterococcus faecalis</i>
371	sea1_1_1	<i>Enterococcus faecalis</i>
372	sep1_1_1	<i>Enterococcus faecalis</i>
373	vicK_1_1	<i>Enterococcus faecalis</i>
374	yycH_1_1	<i>Enterococcus faecalis</i>
375	yycI_1_1	<i>Enterococcus faecalis</i>
376	yycJ_1_1	<i>Enterococcus faecalis</i>
377	bglB_1_1	<i>Enterococcus faecium</i>
378	bglR_1_1	<i>Enterococcus faecium</i>
379	bglS_1_1	<i>Enterococcus faecium</i>
380	efmA_1_1	<i>Enterococcus faecium</i>
381	efmB_1_1	<i>Enterococcus faecium</i>

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SEQ ID NO	Probe name	Template source
382	efmC_1_1	<i>Enterococcus faecium</i>
383	mreC_1_1	<i>Enterococcus faecium</i>
384	mreD_1_1	<i>Enterococcus faecium</i>
385	mvaDEfaecium_1_1	<i>Enterococcus faecium</i>
386	mvaEEfaecium_1_1	<i>Enterococcus faecium</i>
387	mvaK1 Efaecium_1_1	<i>Enterococcus faecium</i>
388	mvaK2Efaecium_1_1	<i>Enterococcus faecium</i>
389	mvaSEfaecium_1_1	<i>Enterococcus faecium</i>
390	orf3_4Efaeciumb_1_1	<i>Enterococcus faecium</i>
391	orf6_7Efaecium_1_1	<i>Enterococcus faecium</i>
392	orf7_8Efaecium_1_1	<i>Enterococcus faecium</i>
393	orf9_10Efaecium_1_1	<i>Enterococcus faecium</i>
394	entA_entl_1_1	<i>Enterococcus faecium</i>
395	entD_1_1	<i>Enterococcus faecium</i>
396	entR_1_1	<i>Enterococcus faecium</i>
397	oep_1_1	<i>Enterococcus faecium</i>
398	sagA_1_2	<i>Enterococcus faecium</i>
399	atsA_1_1	<i>Klebsiella pneumoniae</i>
400	atsB_1_1	<i>Klebsiella pneumoniae</i>
401	budC_1_1	<i>Klebsiella pneumoniae</i>
402	citA_1_1	<i>Klebsiella pneumoniae</i>
403	citW_1_1	<i>Klebsiella pneumoniae</i>
404	citX_1_1	<i>Klebsiella pneumoniae</i>
405	dalD_1_1	<i>Klebsiella pneumoniae</i>
406	dalK_1_1	<i>Klebsiella pneumoniae</i>
407	dalT_1_1	<i>Klebsiella pneumoniae</i>
408	acoA_1_1	<i>Klebsiella pneumoniae</i>
409	acoB_1_1	<i>Klebsiella pneumoniae</i>
410	acoC_1_1	<i>Klebsiella pneumoniae</i>
411	ahIK_1_1	<i>Klebsiella pneumoniae</i>
412	fimK_1_1	<i>Klebsiella pneumoniae</i>
413	glfKPN2_1_1	<i>Klebsiella pneumoniae</i>
414	ltrA_1_1	<i>Klebsiella pneumoniae</i>
415	mdcC_1_1	<i>Klebsiella pneumoniae</i>
416	mdcF_1_1	<i>Klebsiella pneumoniae</i>
417	mdcH_1_1	<i>Klebsiella pneumoniae</i>
418	mrkA_1_1	<i>Klebsiella pneumoniae</i>
419	mtrK_1_1	<i>Klebsiella pneumoniae</i>

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SEQ ID NO	Probe name	Template source
420	nifF_1_1	<i>Klebsiella pneumoniae</i>
421	nifK_1_1	<i>Klebsiella pneumoniae</i>
422	nifN_1_1	<i>Klebsiella pneumoniae</i>
423	tyrP_1_1	<i>Klebsiella pneumoniae</i>
424	ureA_1_1	<i>Klebsiella pneumoniae</i>
425	wbbO_1_1	<i>Klebsiella pneumoniae</i>
426	wza_1_1	<i>Klebsiella pneumoniae</i>
427	wzb_1_1	<i>Klebsiella pneumoniae</i>
428	wzm KPN2_1_1	<i>Klebsiella pneumoniae</i>
429	wztKPN2_1_1	<i>Klebsiella pneumoniae</i>
430	yojH_1_1	<i>Klebsiella pneumoniae</i>
431	liac_1_1	<i>Klebsiella pneumoniae</i>
432	cim_1_1	<i>Klebsiella pneumoniae</i>
433	aldA_1_1	<i>Klebsiella pneumoniae</i>
434	aldA_2_1	<i>Klebsiella pneumoniae</i>
435	hemly_1_1	<i>Klebsiella pneumoniae</i>
436	pSL017_1_1	<i>Klebsiella pneumoniae</i>
437	pSL020_1_1	<i>Klebsiella pneumoniae</i>
438	rcaA_1_1	<i>Klebsiella pneumoniae</i>
439	rmlC_1_1	<i>Klebsiella pneumoniae</i>
440	rmlD_1_1	<i>Klebsiella pneumoniae</i>
441	waaG_1_1	<i>Klebsiella pneumoniae</i>
442	wbbD_1_1	<i>Klebsiella pneumoniae</i>
443	wbbM_1_1	<i>Klebsiella pneumoniae</i>
444	wbbN_1_1	<i>Klebsiella pneumoniae</i>
445	wbdA_1_1	<i>Klebsiella pneumoniae</i>
446	wbdC_1_1	<i>Klebsiella pneumoniae</i>
447	wztKpn_1_1	<i>Klebsiella pneumoniae</i>
448	yibD_1_1	<i>Klebsiella pneumoniae</i>
449	cymA_1_1	<i>Klebsiella oxytoca</i>
450	cymD_1_1	<i>Klebsiella oxytoca</i>
451	cymE_1_1	<i>Klebsiella oxytoca</i>
452	cymH_1_1	<i>Klebsiella oxytoca</i>
453	cymI_1_1	<i>Klebsiella oxytoca</i>
454	cymD_1_1	<i>Klebsiella oxytoca</i>
455	ddrA_1_1	<i>Klebsiella oxytoca</i>
456	fdt-1_1_1	<i>Klebsiella oxytoca</i>
457	fdt-2_1_1	<i>Klebsiella oxytoca</i>

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SEQ ID NO	Probe name	Template source
458	fdt-3_1_1	<i>Klebsiella oxytoca</i>
459	gatY_1_1	<i>Klebsiella oxytoca</i>
460	hydH_1_1	<i>Klebsiella oxytoca</i>
461	masA_1_1	<i>Klebsiella oxytoca</i>
462	nasA_1_1	<i>Klebsiella oxytoca</i>
463	nasE_1_1	<i>Klebsiella oxytoca</i>
464	nasF_1_1	<i>Klebsiella oxytoca</i>
465	pehX_1_1	<i>Klebsiella oxytoca</i>
466	pelX_1_1	<i>Klebsiella oxytoca</i>
467	tagH_1_1	<i>Klebsiella oxytoca</i>
468	tagK_1_1	<i>Klebsiella oxytoca</i>
469	tagT_1_1	<i>Klebsiella oxytoca</i>
470	glpR_1_1	<i>Pseudomonas aeruginosa</i>
471	lasRb_1_1	<i>Pseudomonas aeruginosa</i>
472	OrfX_1_1	<i>Pseudomonas aeruginosa</i>
473	pa0260_1_1	<i>Pseudomonas aeruginosa</i>
474	pa0572_1_1	<i>Pseudomonas aeruginosa</i>
475	pa0625_1_1	<i>Pseudomonas aeruginosa</i>
476	pa0636_1_1	<i>Pseudomonas aeruginosa</i>
477	pa1046_1_1	<i>Pseudomonas aeruginosa</i>
478	pa1069_1_1	<i>Pseudomonas aeruginosa</i>
479	pa1846_1_1	<i>Pseudomonas aeruginosa</i>
480	pa3866_1_1	<i>Pseudomonas aeruginosa</i>
481	pa4082_1_1	<i>Pseudomonas aeruginosa</i>
482	pilAp_1_1	<i>Pseudomonas aeruginosa</i>
483	PilAp2_1_1	<i>Pseudomonas aeruginosa</i>
484	pilC_1_1	<i>Pseudomonas aeruginosa</i>
485	PstP_1_1	<i>Pseudomonas aeruginosa</i>
486	purK_1_1	<i>Pseudomonas aeruginosa</i>
487	uvrDII_1_1	<i>Pseudomonas aeruginosa</i>
488	vsml_1_1	<i>Pseudomonas aeruginosa</i>
489	vsm R_1_2	<i>Pseudomonas aeruginosa</i>
490	xcpX_1_1	<i>Pseudomonas aeruginosa</i>
491	aprA_1_1	<i>Pseudomonas aeruginosa</i>
492	aprE_1_1	<i>Pseudomonas aeruginosa</i>
493	ctx_1_2	<i>Pseudomonas aeruginosa</i>
494	algB_1_1	<i>Pseudomonas aeruginosa</i>
495	algN_1_1	<i>Pseudomonas aeruginosa</i>

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SEQ ID NO	Probe name	Template source
496	algR_1_1	<i>Pseudomonas aeruginosa</i>
497	ExoS_1_1	<i>Pseudomonas aeruginosa</i>
498	fpvA_1_1	<i>Pseudomonas aeruginosa</i>
499	lasRa_1_1	<i>Pseudomonas aeruginosa</i>
500	lipA_1_1	<i>Pseudomonas aeruginosa</i>
501	lipH_1_1	<i>Pseudomonas aeruginosa</i>
502	Orf159_1_2	<i>Pseudomonas aeruginosa</i>
503	Orf252_1_1	<i>Pseudomonas aeruginosa</i>
504	pchG_1_1	<i>Pseudomonas aeruginosa</i>
505	PhzA_1_1	<i>Pseudomonas aeruginosa</i>
506	PhzB_1_1	<i>Pseudomonas aeruginosa</i>
507	PLC_1_1	<i>Pseudomonas aeruginosa</i>
508	plcN_1_1	<i>Pseudomonas aeruginosa</i>
509	plcR_1_1	<i>Pseudomonas aeruginosa</i>
510	pvdD_1_1	<i>Pseudomonas aeruginosa</i>
511	pvdF_1_2	<i>Pseudomonas aeruginosa</i>
512	pyocinS1_1_1	<i>Pseudomonas aeruginosa</i>
513	pyocinS1im_1_1	<i>Pseudomonas aeruginosa</i>
514	pyocinS2_1_1	<i>Pseudomonas aeruginosa</i>
515	pys2_1_1	<i>Pseudomonas aeruginosa</i>
516	pys2_2_1	<i>Pseudomonas aeruginosa</i>
517	rbf303_1_1	<i>Pseudomonas aeruginosa</i>
518	rhlA_1_1	<i>Pseudomonas aeruginosa</i>
519	rhlB_1_1	<i>Pseudomonas aeruginosa</i>
520	rhlR_1_1	<i>Pseudomonas aeruginosa</i>
521	TnAP41_1_2	<i>Pseudomonas aeruginosa</i>
522	toxA_1_1	<i>Pseudomonas aeruginosa</i>
523	cap1EStrpneu_1_1	<i>Streptococcus pneumoniae</i>
524	cap1FStrpneu_1_1	<i>Streptococcus pneumoniae</i>
525	cap1GStrpneu_1_1	<i>Streptococcus pneumoniae</i>
526	cap3AStrpneu_1_1	<i>Streptococcus pneumoniae</i>
527	cap3BStrpneu_1_1	<i>Streptococcus pneumoniae</i>
528	celAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
529	celBStrpneu_1_1	<i>Streptococcus pneumoniae</i>
530	cglAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
531	cglBStrpneu_1_1	<i>Streptococcus pneumoniae</i>
532	cglCStrpneu_1_1	<i>Streptococcus pneumoniae</i>
533	cglDStrpneu_1_1	<i>Streptococcus pneumoniae</i>

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SEQ ID NO	Probe name	Template source
534	cinA_1_1	<i>Streptococcus pneumoniae</i>
535	cps14EStrpneum_1_1	<i>Streptococcus pneumoniae</i>
536	cps14FStrpneum_1_1	<i>Streptococcus pneumoniae</i>
537	cps14GStrpneum_1_1	<i>Streptococcus pneumoniae</i>
538	cps14HStrpneum_1_1	<i>Streptococcus pneumoniae</i>
539	cps19aHStrpneum_1_1	<i>Streptococcus pneumoniae</i>
540	cps19aIStrpneum_1_1	<i>Streptococcus pneumoniae</i>
541	cps19aKStrpneum_1_1	<i>Streptococcus pneumoniae</i>
542	cps19fGStrpneum_1_1	<i>Streptococcus pneumoniae</i>
543	cps23fGStrpneum_1_1	<i>Streptococcus pneumoniae</i>
544	dexB_1_1	<i>Streptococcus pneumoniae</i>
545	dinF_1_1	<i>Streptococcus pneumoniae</i>
546	1760Strpneu_1_1	<i>Streptococcus pneumoniae</i>
547	acyPStrpneu_1_1	<i>Streptococcus pneumoniae</i>
548	endAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
549	exoAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
550	exp72_1_1	<i>Streptococcus pneumoniae</i>
551	fnlAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
552	fnlBStrpneu_1_1	<i>Streptococcus pneumoniae</i>
553	fnlCStrpneu_1_1	<i>Streptococcus pneumoniae</i>
554	gct18Strpneum_1_1	<i>Streptococcus pneumoniae</i>
555	hexB1_1_1	<i>Streptococcus pneumoniae</i>
556	hftsHstrpneu_1_1	<i>Streptococcus pneumoniae</i>
557	immunofrag 1 Strpneu_1_1	<i>Streptococcus pneumoniae</i>
558	immunofrag2Strpneu_2_1	<i>Streptococcus pneumoniae</i>
559	immunofrag3Strpneu_2_1	<i>Streptococcus pneumoniae</i>
560	kdtBStrpneu_1_1	<i>Streptococcus pneumoniae</i>
561	lysAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
562	pcpBStrpneu_1_1	<i>Streptococcus pneumoniae</i>
563	pflCStrpneu_1_1	<i>Streptococcus pneumoniae</i>
564	plpA_1_1	<i>Streptococcus pneumoniae</i>
565	prtA1Strpneu_1_1	<i>Streptococcus pneumoniae</i>
566	pspC1Strpneu_1_1	<i>Streptococcus pneumoniae</i>
567	pspC2_1_1	<i>Streptococcus pneumoniae</i>
568	purRStrpneu_1_1	<i>Streptococcus pneumoniae</i>
569	pyrDAStrpneum_1_1	<i>Streptococcus pneumoniae</i>
570	SP0828Strpneu_1_1	<i>Streptococcus pneumoniae</i>
571	SP0830Strpneu_1_1	<i>Streptococcus pneumoniae</i>

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SEQ ID NO	Probe name	Template source
572	SP0833Strpneu_1_1	<i>Streptococcus pneumoniae</i>
573	SP0837_38Strpneu_1_1	<i>Streptococcus pneumoniae</i>
574	SP0839Strpneu_1_1	<i>Streptococcus pneumoniae</i>
575	ugdStrpneu_1_1	<i>Streptococcus pneumoniae</i>
576	uncC_1_1	<i>Streptococcus pneumoniae</i>
577	vicXStrpneu_1_1	<i>Streptococcus pneumoniae</i>
578	wchA6bStrpneum_1_1	<i>Streptococcus pneumoniae</i>
579	wci4Strpneum_1_1	<i>Streptococcus pneumoniae</i>
580	wciK4Strpneum_1_1	<i>Streptococcus pneumoniae</i>
581	wciL4Strpneum_1_1	<i>Streptococcus pneumoniae</i>
582	wciN6bStrpneum_1_1	<i>Streptococcus pneumoniae</i>
583	wciO6bStrpneum_1_1	<i>Streptococcus pneumoniae</i>
584	wciP6bStrpneum_1_1	<i>Streptococcus pneumoniae</i>
585	wciY18Strpneum_1_1	<i>Streptococcus pneumoniae</i>
586	wzdbStrpneum_1_1	<i>Streptococcus pneumoniae</i>
587	wze6bStrpneum_1_1	<i>Streptococcus pneumoniae</i>
588	wzy18Strpneum_1_1	<i>Streptococcus pneumoniae</i>
589	wzy4Strpneum_1_1	<i>Streptococcus pneumoniae</i>
590	wzy6bStrpneum_1_1	<i>Streptococcus pneumoniae</i>
591	xpt_1_1	<i>Streptococcus pneumoniae</i>
592	igaStrpneu_1_1	<i>Streptococcus pneumoniae</i>
593	lytA_1_1	<i>Streptococcus pneumoniae</i>
594	nanA_1_1	<i>Streptococcus pneumoniae</i>
595	nanBStrpneu_1_1	<i>Streptococcus pneumoniae</i>
596	pcpCStrpneu_1_1	<i>Streptococcus pneumoniae</i>
597	ply_1_1	<i>Streptococcus pneumoniae</i>
598	prtAStrpneu_1_1	<i>Streptococcus pneumoniae</i>
599	pspA_1_2	<i>Streptococcus pneumoniae</i>
600	SP0834Strpneu_1_1	<i>Streptococcus pneumoniae</i>
601	SP0834Strpneu_1_2	<i>Streptococcus pneumoniae</i>
602	sphtraStrpneu_1_1	<i>Streptococcus pneumoniae</i>
603	wciJStrpneu_1_1	<i>Streptococcus pneumoniae</i>
604	wziyStrpneu_1_1	<i>Streptococcus pneumoniae</i>
605	wzxStrpneu_1_1	<i>Streptococcus pneumoniae</i>
606	cpsA1Strgal_1_1	<i>Streptococcus agalactiae</i>
607	cpsB1 Strgal_1_1	<i>Streptococcus agalactiae</i>
608	cpsC1Strgal_1_1	<i>Streptococcus agalactiae</i>
609	cpsD1Strgal_1_1	<i>Streptococcus agalactiae</i>

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SEQ ID NO	Probe name	Template source
610	cpsE1Strgal_1_1	<i>Streptococcus agalactiae</i>
611	cpsG1Strgal_1_1	<i>Streptococcus agalactiae</i>
612	cpsI1Strgal_1_1	<i>Streptococcus agalactiae</i>
613	cpsJ1Strgal_1_1	<i>Streptococcus agalactiae</i>
614	cpsK1Strgal_1_1	<i>Streptococcus agalactiae</i>
615	cpsM1Strgal_1_1	<i>Streptococcus agalactiae</i>
616	cpsY1Strgal_1_1	<i>Streptococcus agalactiae</i>
617	cpsY2Strgal_2_1	<i>Streptococcus agalactiae</i>
618	cylB1Straga_1_1	<i>Streptococcus agalactiae</i>
619	cylE1Straga_1_1	<i>Streptococcus agalactiae</i>
620	cylF1Straga_1_1	<i>Streptococcus agalactiae</i>
621	cylH1Straga_1_1	<i>Streptococcus agalactiae</i>
622	cylI1Straga_1_1	<i>Streptococcus agalactiae</i>
623	cylJ1Straga_1_1	<i>Streptococcus agalactiae</i>
624	cylK1Straga_1_1	<i>Streptococcus agalactiae</i>
625	0487Straga_1_1	<i>Streptococcus agalactiae</i>
626	0488Straga_1_1	<i>Streptococcus agalactiae</i>
627	0493Straga_1_1	<i>Streptococcus agalactiae</i>
628	0495Straga_1_1	<i>Streptococcus agalactiae</i>
629	0498Straga_1_1	<i>Streptococcus agalactiae</i>
630	0500Straga_1_1	<i>Streptococcus agalactiae</i>
631	0502Straga_1_1	<i>Streptococcus agalactiae</i>
632	0504Straga_1_1	<i>Streptococcus agalactiae</i>
633	folD1Straga_1_1	<i>Streptococcus agalactiae</i>
634	neuA1Strgal_1_1	<i>Streptococcus agalactiae</i>
635	neuB1Strgal_1_1	<i>Streptococcus agalactiae</i>
636	neuC1Strgal_1_1	<i>Streptococcus agalactiae</i>
637	neuD1Strgal_1_1	<i>Streptococcus agalactiae</i>
638	recN1Straga_1_1	<i>Streptococcus agalactiae</i>
639	ileS1Straga_1_1	<i>Streptococcus agalactiae</i>
640	CAMPfactor_1_1	<i>Streptococcus agalactiae</i>
641	CAMPfactor_2_1	<i>Streptococcus agalactiae</i>
642	0499Straga_1_1	<i>Streptococcus agalactiae</i>
643	hyl1Stragal_1_1	<i>Streptococcus agalactiae</i>
644	lip1Stragal_1_1	<i>Streptococcus agalactiae</i>
645	cycl1Strpyog_1_1	<i>Streptococcus pyogenes</i>
646	fah_rph_hlo_Strpyog_1_1	<i>Streptococcus pyogenes</i>
647	int_1_1	<i>Streptococcus pyogenes</i>

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SEQ ID NO	Probe name	Template source
648	int315.5_1_1	<i>Streptococcus pyogenes</i>
649	murEStrpyog_1_1	<i>Streptococcus pyogenes</i>
650	oppA_1_1	<i>Streptococcus pyogenes</i>
651	oppCStrpyog_1_1	<i>Streptococcus pyogenes</i>
652	oppD_1_1	<i>Streptococcus pyogenes</i>
653	SPy0382Strpyog_1_1	<i>Streptococcus pyogenes</i>
654	SPy0390Strpyog_1_1	<i>Streptococcus pyogenes</i>
655	SPyM3_1351_1_1	<i>Streptococcus pyogenes</i>
656	vicXStrpyog_1_1	<i>Streptococcus pyogenes</i>
657	DNaseIStrpyog_1_1	<i>Streptococcus pyogenes</i>
658	fba2Strpyog_1_1	<i>Streptococcus pyogenes</i>
659	fhuAStrpyog_1_1	<i>Streptococcus pyogenes</i>
660	fhuBStrpyog_1_1	<i>Streptococcus pyogenes</i>
661	fhuDStrpyog_1_1	<i>Streptococcus pyogenes</i>
662	fhuGStrpyog_1_1	<i>Streptococcus pyogenes</i>
663	hylA_1_1	<i>Streptococcus pyogenes</i>
664	hylP_1_1	<i>Streptococcus pyogenes</i>
665	hylP2_1_1	<i>Streptococcus pyogenes</i>
666	oppB_1_1	<i>Streptococcus pyogenes</i>
667	ropB_1_1	<i>Streptococcus pyogenes</i>
668	scpAStrpyog_1_1	<i>Streptococcus pyogenes</i>
669	sloStrpyog_1_1	<i>Streptococcus pyogenes</i>
670	smez-4Strpyog_1_1	<i>Streptococcus pyogenes</i>
671	sof_1_1	<i>Streptococcus pyogenes</i>
672	sof_2_1	<i>Streptococcus pyogenes</i>
673	speA_1_1	<i>Streptococcus pyogenes</i>
674	speB2Strpyog_1_1	<i>Streptococcus pyogenes</i>
675	speCStrpyog_1_1	<i>Streptococcus pyogenes</i>
676	speJStrpyog_1_1	<i>Streptococcus pyogenes</i>
677	srtBStrpyog_1_1	<i>Streptococcus pyogenes</i>
678	srtCStrpyog_1_1	<i>Streptococcus pyogenes</i>
679	srtEStrpyog_1_1	<i>Streptococcus pyogenes</i>
680	srtFStrpyog_1_1	<i>Streptococcus pyogenes</i>
681	srtGStrpyog_1_1	<i>Streptococcus pyogenes</i>
682	srtIStrpyog_1_1	<i>Streptococcus pyogenes</i>
683	srtKStrpyog_1_1	<i>Streptococcus pyogenes</i>
684	srtRStrpyog_1_1	<i>Streptococcus pyogenes</i>
685	srtTStrpyog_1_1	<i>Streptococcus pyogenes</i>

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SEQ ID NO	Probe name	Template source
686	vicKStrpyog_1_1	<i>Streptococcus pyogenes</i>
687	573SStprmut_1_1	<i>Streptococcus viridans</i>
688	580SSStprmut_1_1	<i>Streptococcus viridans</i>
689	581_582SSStprmut_1_1	<i>Streptococcus viridans</i>
690	584SSStprmut_1_1	<i>Streptococcus viridans</i>
691	dltAStmut_1_1	<i>Streptococcus viridans</i>
692	dltBStmut_1_1	<i>Streptococcus viridans</i>
693	dltCpx1Stmut_1_1	<i>Streptococcus viridans</i>
694	dltDStmut_1_1	<i>Streptococcus viridans</i>
695	lichStrbov_1_1	<i>Streptococcus viridans</i>
696	lytRStprmut_1_1	<i>Streptococcus viridans</i>
697	lytSStprmut_1_1	<i>Streptococcus viridans</i>
698	pepQStmut_1_1	<i>Streptococcus viridans</i>
699	pflCStmut_1_1	<i>Streptococcus viridans</i>
700	recNStprmut_1_1	<i>Streptococcus viridans</i>
701	ytqBStmut_1_1	<i>Streptococcus viridans</i>
702	hlyXStmut_1_1	<i>Streptococcus viridans</i>
703	igaStrmitis_1_1	<i>Streptococcus viridans</i>
704	igaStrsanguis_1_1	<i>Streptococcus viridans</i>
705	perMStmut_1_1	<i>Streptococcus viridans</i>
706	atfA_1_1	<i>Proteus mirabilis</i>
707	atfB_1_1	<i>Proteus mirabilis</i>
708	atfC_1_1	<i>Proteus mirabilis</i>
709	ccmPrmi1_1_1	<i>Proteus mirabilis</i>
710	cyaPrmi_1_1	<i>Proteus mirabilis</i>
711	aad_1_1	<i>Proteus mirabilis</i>
712	flfB_1_1	<i>Proteus mirabilis</i>
713	flfD_1_1	<i>Proteus mirabilis</i>
714	flfN_1_1	<i>Proteus mirabilis</i>
715	flhD_1_1	<i>Proteus mirabilis</i>
716	floA_1_1	<i>Proteus mirabilis</i>
717	ftsK_1_1	<i>Proteus mirabilis</i>
718	gstB_1_1	<i>Proteus mirabilis</i>
719	hem CPrmi_1_1	<i>Proteus mirabilis</i>
720	hem DPrmi_1_1	<i>Proteus mirabilis</i>
721	hev_1_1	<i>Proteus mirabilis</i>
722	katA_1_1	<i>Proteus mirabilis</i>
723	lpp1_1_1	<i>Proteus mirabilis</i>

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SEQ ID NO	Probe name	Template source
724	menE_1_1	<i>Proteus mirabilis</i>
725	mfd_1_1	<i>Proteus mirabilis</i>
726	nrpA_1_1	<i>Proteus mirabilis</i>
727	nrpB_1_1	<i>Proteus mirabilis</i>
728	nrpG_1_1	<i>Proteus mirabilis</i>
729	nrpS_1_1	<i>Proteus mirabilis</i>
730	nrpT_1_1	<i>Proteus mirabilis</i>
731	nrpU_1_1	<i>Proteus mirabilis</i>
732	pat_1_1	<i>Proteus mirabilis</i>
733	pmfA_1_1	<i>Proteus mirabilis</i>
734	pmfC_1_1	<i>Proteus mirabilis</i>
735	pmfE_1_1	<i>Proteus mirabilis</i>
736	ppaA_1_1	<i>Proteus mirabilis</i>
737	rsbA_1_1	<i>Proteus mirabilis</i>
738	rsbC_1_1	<i>Proteus mirabilis</i>
739	speB_1_1	<i>Proteus mirabilis</i>
740	stmA_1_1	<i>Proteus mirabilis</i>
741	stmB_1_1	<i>Proteus mirabilis</i>
742	terA_1_1	<i>Proteus mirabilis</i>
743	terD_1_1	<i>Proteus mirabilis</i>
744	umoA_1_1	<i>Proteus mirabilis</i>
745	umoB_1_1	<i>Proteus mirabilis</i>
746	umoC_1_1	<i>Proteus mirabilis</i>
747	ureR_1_1	<i>Proteus mirabilis</i>
748	xerC_1_1	<i>Proteus mirabilis</i>
749	ygbA_1_1	<i>Proteus mirabilis</i>
750	flaA_1_1	<i>Proteus mirabilis</i>
751	flaD_1_1	<i>Proteus mirabilis</i>
752	fliA_1_1	<i>Proteus mirabilis</i>
753	hpmA_1_1	<i>Proteus mirabilis</i>
754	hpmB_1_1	<i>Proteus mirabilis</i>
755	lpsPrmi_1_1	<i>Proteus mirabilis</i>
756	mrpA_1_1	<i>Proteus mirabilis</i>
757	mrpB_1_1	<i>Proteus mirabilis</i>
758	mrpC_1_1	<i>Proteus mirabilis</i>
759	mrpD_1_1	<i>Proteus mirabilis</i>
760	mrpE_1_1	<i>Proteus mirabilis</i>
761	mrpF_1_1	<i>Proteus mirabilis</i>

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SEQ ID NO	Probe name	Template source
762	mrpG_1_1	<i>Proteus mirabilis</i>
763	mrpH_1_1	<i>Proteus mirabilis</i>
764	mrpI_1_1	<i>Proteus mirabilis</i>
765	mrpJ_1_1	<i>Proteus mirabilis</i>
766	patA_1_1	<i>Proteus mirabilis</i>
767	putA_1_1	<i>Proteus mirabilis</i>
768	uca_1_1	<i>Proteus mirabilis</i>
769	ureDPmi_1_1	<i>Proteus mirabilis</i>
770	ureEPmi_1_1	<i>Proteus mirabilis</i>
771	ureFPmi_1_1	<i>Proteus mirabilis</i>
772	zapA_1_1	<i>Proteus mirabilis</i>
773	zapB_1_1	<i>Proteus mirabilis</i>
774	zapD_1_1	<i>Proteus mirabilis</i>
775	zapE_1_1	<i>Proteus mirabilis</i>
776	envZPrvu_1_1	<i>Proteus vulgaris</i>
777	frdC_1_1	<i>Proteus vulgaris</i>
778	frdD_1_1	<i>Proteus vulgaris</i>
779	infBPrvu_1_1	<i>Proteus vulgaris</i>
780	lad_1_1	<i>Proteus vulgaris</i>
781	tna2_1_1	<i>Proteus vulgaris</i>
782	end_1_1	<i>Proteus vulgaris</i>
783	pqrA_1_1	<i>Proteus vulgaris</i>
784	urg_1_1	<i>Proteus vulgaris</i>
785	blaIMP-7_1_1	<i>Pseudomonas aeruginosa</i>
786	mecISepid_1_1	<i>Staphylococcus epidermidis</i>
787	blaOXA-10_1_2	<i>Pseudomonas aeruginosa</i>
788	blaB_1_1	<i>Proteus vulgaris</i>
789	ampC_1_1	<i>Klebsiella oxytoca</i>
790	I-blaR_1_1	<i>Staphylococcus aureus</i>
791	blaOXA-32_1_1	<i>Pseudomonas aeruginosa</i>
792	bla- CTX-M-22_1_1	<i>Klebsiella pneumoniae</i>
793	pbp2aStrpneu_1_1	<i>Streptococcus pneumoniae</i>
794	blaSHV-1_1_1	<i>Klebsiella pneumoniae</i>
795	blaOXA-2_1_1	<i>Salmonella typhimurium</i>
796	blaRShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
797	blaIMP-7_1_2	<i>Pseudomonas aeruginosa</i>
798	I-mecR_1_1	<i>Staphylococcus aureus</i>
799	blaOXY_1_1	<i>Klebsiella oxytoca</i>

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SEQ ID NO	Probe name	Template source
800	dacCStrpyog_1_1	<i>Streptococcus pyogenes</i>
801	femA_1_1	<i>Staphylococcus aureus</i>
802	mecA_1_1	<i>Staphylococcus aureus</i>
803	blaShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
804	blavim_1_1	<i>Pseudomonas aeruginosa</i>
805	pbp2b_1_1	<i>Streptococcus pneumoniae</i>
806	pbp2primeSepid_1_1	<i>Staphylococcus epidermidis</i>
807	pbp2x_1_1	<i>Streptococcus pneumoniae</i>
808	pbp3Saureuc_1_1	<i>Staphylococcus aureus</i>
809	pbp4_1_1	<i>Enterococcus faecalis</i>
810	pbp5Efaecium_1_1	<i>Enterococcus faecium</i>
811	pbpC_1_1	<i>Enterococcus faecalis</i>
812	l-mecI_1_1	<i>Staphylococcus aureus</i>
813	pbp1a_1_1	<i>Streptococcus pneumoniae</i>
814	l-blaI_1_1	<i>Staphylococcus aureus</i>
815	blaTEM-106_1_1	<i>Escherichia coli</i>
816	blaOXY-KLOX_1_1	<i>Klebsiella oxytoca</i>
817	ftsWEF_1_1	<i>Enterococcus faecium</i>
818	fmhB_1_1	<i>Staphylococcus aureus</i>
819	cumA_1_1	<i>Proteus vulgaris</i>
820	femBShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
821	blaPER-1_1_1	<i>Pseudomonas aeruginosa</i>
822	bla_FOX-3_1_1	<i>Klebsiella oxytoca</i>
823	blaA_1_1	<i>Proteus vulgaris</i>
824	psrb_1_1	<i>Enterococcus faecium</i>
825	fmhA_1_1	<i>Staphylococcus aureus</i>
826	mecR1Sepid_1_1	<i>Staphylococcus epidermidis</i>
827	blaZ_1_1	<i>Staphylococcus aureus</i>
828	blaOXA-1_1_1	<i>Plasmid FGN238</i>
829	fox-6_1_1	<i>Klebsiella pneumoniae</i>
830	blaPrmi_1_1	<i>Proteus mirabilis</i>
831	aacA_aphDStwar_1_1	<i>Staphylococcus warneri</i>
832	aacC1_1_2	<i>Pseudomonas aeruginosa</i>
833	aacC2_1_1	<i>Escherichia coli</i>
834	strB_1_1	<i>Escherichia coli</i>
835	aadA_1_1	<i>Enterococcus faecalis</i>
836	aadB_1_2	<i>Escherichia coli</i>
837	aadD_1_1	<i>Staphylococcus aureus</i>

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SEQ ID NO	Probe name	Template source
838	aacA4_1_2	<i>Pseudomonas aeruginosa</i>
839	strA_1_1	<i>Escherichia coli</i>
840	aph-A3_1_1	<i>Staphylococcus aureus</i>
841	aacC1_1_1	<i>Pseudomonas aeruginosa</i>
842	aacA4_1_1	<i>Pseudomonas aeruginosa</i>
843	aacA-aphD_1_1	<i>Staphylococcus aureus</i>
844	l-spc_1_1	<i>Staphylococcus aureus</i>
845	aphA3_1_1	<i>synthetic construct</i>
846	ermC_1_1	<i>Staphylococcus aureus</i>
847	linB_1_1	<i>Enterococcus faecium</i>
848	satSA_1_1	<i>Staphylococcus aureus</i>
849	mdrSA_1_1	<i>Staphylococcus aureus</i>
850	l-linA_1_1	<i>Staphylococcus aureus</i>
851	erm B_1_2	<i>Staphylococcus aureus</i>
852	ermA_1_1	<i>Staphylococcus aureus</i>
853	satA_1_1	<i>Enterococcus faecium</i>
854	msrA_1_1	<i>Staphylococcus aureus</i>
855	mphBM_1_1	<i>Staphylococcus aureus</i>
856	mefA_1_1	<i>Streptococcus pyogenes</i>
857	mrX_1_1	<i>Escherichia coli</i>
858	dfrStrpneu_1_1	<i>Streptococcus pneumoniae</i>
859	dfrA_1_1	<i>Staphylococcus aureus</i>
860	cm IA5_1_1	<i>Escherichia coli</i>
861	catEfaecium_1_1	<i>Enterococcus faecium</i>
862	cat_1_1	<i>Staphylococcus aureus</i>
863	tetAJ_1_1	<i>Proteus mirabilis</i>
864	tetL_1_1	<i>Enterococcus faecalis</i>
865	tetM_1_1	<i>Enterococcus faecalis</i>
866	vanH(tn)_1_1	<i>Enterococcus faecium</i>
867	vanA_1_1	<i>Enterococcus faecium</i>
868	vanHB2_1_1	<i>Enterococcus faecium</i>
869	vanR_1_1	<i>Enterococcus faecium</i>
870	vanRB2_1_1	<i>Enterococcus faecium</i>
871	vanS(tn)_1_1	<i>Enterococcus faecium</i>
872	vanSB2_1_1	<i>Enterococcus faecium</i>
873	vanWB2_1_1	<i>Enterococcus faecium</i>
874	ddl_1_1	<i>Enterococcus faecalis</i>
875	ble_1_1	<i>Staphylococcus aureus</i>

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SEQ ID NO	Probe name	Template source
876	vanXB2_1_1	<i>Enterococcus faecium</i>
877	vanY(tn)_1_1	<i>Enterococcus faecium</i>
878	vanYB2_1_1	<i>Enterococcus faecium</i>
879	vanB_1_1	<i>Enterococcus faecalis</i>
880	vanZ(tn)_1_1	<i>Enterococcus faecium</i>
881	vanC-2_1_1	<i>Enterococcus flavescens</i>
882	vanX(tn)_1_1	<i>Enterococcus faecium</i>
883	acrB_1_1	<i>Proteus mirabilis</i>
884	mexB_1_2	<i>Pseudomonas aeruginosa</i>
885	l-qacA_1_1	<i>Staphylococcus aureus</i>
886	sull_1_1	<i>Escherichia coli</i>
887	sul_1_1	<i>Escherichia coli</i>
888	cadBStalugd_1_1	<i>Staphylococcus lugdunensis</i>
889	mexA_1_1	<i>Pseudomonas aeruginosa</i>
890	acrR_1_1	<i>Proteus mirabilis</i>
891	emeA_1_1	<i>Enterococcus faecalis</i>
892	acrA_1_1	<i>Proteus mirabilis</i>
893	rtn_1_1	<i>Proteus vulgaris</i>
894	abcXStrpmut_1_1	<i>Streptococcus mutans</i>
895	qacEdelta1_1_1	<i>Escherichia coli</i>
896	elkT-abcA_1_1	<i>Staphylococcus aureus</i>
897	l-cadA_1_1	<i>Staphylococcus aureus</i>
898	albA_1_1	<i>Klebsiella oxytoca</i>
899	wzm_1_1	<i>Klebsiella pneumoniae</i>
900	msrCb_1_1	<i>Enterococcus faecium</i>
901	nov_1_1	<i>Escherichia coli</i>
902	wzt_1_1	<i>Klebsiella pneumoniae</i>
903	wbbl_1_1	<i>Klebsiella pneumoniae</i>
904	norA23_1_1	<i>Staphylococcus aureus</i>
905	mexR_1_1	<i>Pseudomonas aeruginosa</i>
906	arr2_1_1	<i>Escherichia coli</i>
907	mreA_1_1	<i>Staphylococcus aureus</i>
908	l-cadC_1_1	<i>Staphylococcus aureus</i>
909	uvrA_1_1	<i>Enterococcus faecalis</i>
910	CRD2_1_1	<i>Candida albicans</i>
911	CDR1_1_1	<i>Candida albicans</i>
912	CDR1_2_1	<i>Candida albicans</i>
913	MET3_1_1	<i>Candida albicans</i>

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SEQ ID NO	Probe name	Template source
914	FET3_1_1	<i>Candida albicans</i>
915	FTR2_1_1	<i>Candida albicans</i>
916	MDR1-7_1_1	<i>Candida albicans</i>
917	ERG11_1_1	<i>Candida albicans</i>
918	SEC20_1_1	<i>Candida albicans</i>
919	rbcL_1_1	<i>Glycine max</i>
920	LDHA(hu)_1_1	<i>Homo sapiens</i>
921	GAPD(hu)_1_1	<i>Homo sapiens</i>
922	b-Act(hu)_1_1	<i>Homo sapiens</i>
923	ARHGDIA(hu)_1_1	<i>Homo sapiens</i>
924	PGK1(hu)_1_1	<i>Homo sapiens</i>
925	rbcL_1_2	<i>Glycine max</i>
926	16SPa_1_1	<i>Pseudomonas aeruginosa</i>
927	23SEfaecium_2_1	<i>Enterococcus faecium</i>
928	16SSStrepog_1_1	<i>Streptococcus pyogenes</i>
929	16SSStrepneu_1_1	<i>Streptococcus pneumoniae</i>
930	16SSStrepagalactiae_1_1	<i>Streptococcus agalactiae</i>
931	16SEfaecium_1_1	<i>Enterococcus faecium</i>
932	16SEfaecium_2_1	<i>Enterococcus faecium</i>
933	16SRNAEf_2_1	<i>Enterococcus faecalis</i>
934	16SKpn_1_1	<i>Klebsiella pneumoniae</i>
935	16SSa_3_1	<i>Staphylococcus aureus</i>
936	16SRNAEf_1_1	<i>Enterococcus faecalis</i>
937	16SShominis_1_1	<i>Staphylococcus hominis</i>
938	16SShaemolyt_1_1	<i>Staphylococcus haemolyticus</i>
939	23SEfaecium_1_1	<i>Enterococcus faecium</i>
940	16SrRNAPrmi_1_1	<i>Proteus mirabilis</i>
941	16SrRNAPrvu1_1_1	<i>Proteus vulgaris</i>
942	16SSa_1_1	<i>Staphylococcus aureus</i>
943	16SKlox_1_1	<i>Klebsiella oxytoca</i>
944	p53_1_1	<i>Mus musculus</i>
945	0135mihck_1_1	<i>Dictyostelium discoideum</i>
946	FAN_1_1	<i>Mus musculus</i>
947	0270cap_1_1	<i>Dictyostelium discoideum</i>

b) primer sequences

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SEQ ID NO	Probe name	Direction
948	cataSaur_1_1	F(oward)
949	cataSaur_1_1	R(everse)
950	cataSaur_1_2	F
951	cataSaur_1_2	R
952	clfA_1_1	F
953	clfA_1_1	R
954	clfB_1_1	F
955	clfB_1_1	R
956	coa_1_1	F
957	coa_1_1	R
958	coa_1_2	F
959	coa_1_2	R
960	l-clpC_1_1	F
961	l-clpC_1_1	R
962	l-clpP_1_1	F
963	l-clpP_1_1	R
964	l-ctaA_1_1	F
965	l-ctaA_1_1	R
966	l-ctsR_1_1	F
967	l-ctsR_1_1	R
968	l-dltA_1_1	F
969	l-dltA_1_1	R
970	l-dltB_1_1	F
971	l-dltB_1_1	R
972	l-dltC_1_1	F
973	l-dltc_1_1	R
974	l-dnaK_1_1	F
975	l-dnaK_1_1	R
976	l-elkT_1_1	F
977	l-elkT_1_1	R
978	l-femD_1_1	F
979	l-femD_1_1	R
980	l-glnA_1_1	F
981	l-glnA_1_1	R
982	l-glnR_1_1	F
983	l-glnR_1_1	R
984	l-grlA_1_1	F
985	l-grlA_1_1	R
986	l-grlB_1_1	F

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SEQ ID NO	Probe name	Direction
987	I-grlB_1_1	R
988	I-groEL_1_1	F
989	I-groEL_1_1	R
990	I-groES_1_1	F
991	I-groES_1_1	R
992	I-hemA_1_1	F
993	I-hemA_1_1	R
994	I-hemE_1_1	F
995	I-hemE_1_1	R
996	I-hemH_1_1	F
997	I-hemH_1_1	R
998	I-hemL_1_1	F
999	I-hemL_1_1	R
1000	I-hemY_1_1	F
1001	I-hemY_1_1	R
1002	I-lepA_1_1	F
1003	I-lepA_1_1	R
1004	I-lrgA_1_1	F
1005	I-lrgA_1_1	R
1006	I-lrgB_1_1	F
1007	I-lrgB_1_1	R
1008	I-lytM_1_1	F
1009	I-lytM_1_1	R
1010	I-menB_1_1	F
1011	I-menB_1_1	R
1012	I-menD_1_1	F
1013	I-menD_1_1	R
1014	I-menE_1_1	F
1015	I-menE_1_1	R
1016	I-menF_1_1	F
1017	I-menF_1_1	R
1018	I-mreB_1_1	F
1019	I-mreB_1_1	R
1020	I-mreR_1_1	F
1021	I-mreR_1_1	R
1022	I-mutL_1_1	F
1023	I-mutL_1_1	R
1024	I-mutS_1_1	F

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SEQ ID NO	Probe name	Direction
1025	l-mutS_1_1	R
1026	l-NAG_1_1	F
1027	l-NAG_1_1	R
1028	l-pbg_1_1	F
1029	l-pbg_1_1	R
1030	l-pbpF_1_1	F
1031	l-pbpF_1_1	R
1032	l-pdhB_1_1	F
1033	l-pdhB_1_1	R
1034	l-pdhC_1_1	F
1035	l-pdhC_1_1	R
1036	l-rsbU_1_1	F
1037	l-rsbU_1_1	R
1038	l-rsbV_1_1	F
1039	l-rsbV_1_1	R
1040	l-rsbW_1_1	F
1041	l-rsbW_1_1	R
1042	l-sgp_1_1	F
1043	l-sgp_1_1	R
1044	l-sirR_1_1	F
1045	l-sirR_1_1	R
1046	l-sodA_1_1	F
1047	l-sodA_1_1	R
1048	l-sodB_1_1	F
1049	l-sodB_1_1	R
1050	l-sstA_1_1	F
1051	l-sstA_1_1	R
1052	l-sstB_1_1	F
1053	l-sstB_1_1	R
1054	l-sstC_1_1	F
1055	l-sstC_1_1	R
1056	l-sstD_1_1	F
1057	l-sstD_1_1	R
1058	l-trx_1_1	F
1059	l-trx_1_1	R
1060	l-yhiN_1_1	F
1061	l-yhiN_1_1	R
1062	epiP-bsaP_1_1	F

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SEQ ID NO	Probe name	Direction
1063	epiP-bsaP_1_1	R
1064	geh_1_1	F
1065	geh_1_1	R
1066	gyrA_1_1	F
1067	gyrA_1_1	R
1068	gyrB_1_1	F
1069	gyrB_1_1	R
1070	hemB_1_1	F
1071	hemB_1_1	R
1072	hemC_1_1	F
1073	hemC_1_1	R
1074	hemD_1_1	F
1075	hemD_1_1	R
1076	hemN_1_1	F
1077	hemN_1_1	R
1078	hsdS_1_1	F
1079	hsdS_1_1	R
1080	hsdS_2_1	F
1081	hsdS_2_1	R
1082	lip_1_1	F
1083	lip_1_1	R
1084	menC_1_1	F
1085	menC_1_1	R
1086	murC_1_1	F
1087	murC_1_1	R
1088	nuc_1_1	F
1089	nuc_1_1	R
1090	pdhD_1_1	F
1091	pdhD_1_1	R
1092	rpoB_1_1	F
1093	rpoB_1_1	R
1094	SAV0431_1_1	F
1095	SAV0431_1_1	R
1096	SAV0439_1_1	F
1097	SAV0439_1_1	R
1098	SAV0440_1_1	F
1099	SAV0440_1_1	R
1100	SAV0441_1_1	F

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SEQ ID NO	Probe name	Direction
1101	SAV0441_1_1	R
1102	sigB_1_1	F
1103	sigB_1_1	R
1104	spa_1_2	F
1105	spa_1_2	R
1106	sstC_1_1	F
1107	sstC_1_1	R
1108	tag_1_1	F
1109	tag_1_1	R
1110	tyrA_1_1	F
1111	tyrA_1_1	R
1112	l-aroC_1_1	F
1113	l-aroC_1_1	R
1114	l-aroA_1_1	F
1115	l-aroA_1_1	R
1116	l-cna_1_1	F
1117	l-cna_1_1	R
1118	l-ebpS_1_1	F
1119	l-ebpS_1_1	R
1120	l-eno_1_1	F
1121	l-eno_1_1	R
1122	l-fbpA_1_1	F
1123	l-fbpA_1_1	R
1124	l-fib_1_1	F
1125	l-fib_1_1	R
1126	l-fnbB_1_1	F
1127	l-fnbB_1_1	R
1128	l-srtA_1_1	F
1129	l-srtA_1_1	R
1130	l-stpC_1_1	F
1131	l-stpC_1_1	R
1132	l-fnbA_1_1	F
1133	l-fnbA_1_1	R
1134	l-spa_1_1	F
1135	l-spa_1_1	R
1136	l-aroE_1_1	F
1137	l-aroE_1_1	R
1138	l-aroF_1_1	F

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SEQ ID NO	Probe name	Direction
1139	l-aroF_1_1	R
1140	l-aroG_1_1	F
1141	l-aroG_1_1	R
1142	l-asp23_1_1	F
1143	l-asp23_1_1	R
1144	l-atl_1_1	F
1145	l-atl_1_1	R
1146	bsaE_1_1	F
1147	bsaE_1_1	R
1148	bsaG_1_1	F
1149	bsaG_1_1	R
1150	cap5h_1_1	F
1151	cap5h_1_1	R
1152	cap5i_1_1	F
1153	cap5i_1_1	R
1154	cap5j_1_1	F
1155	cap5j_1_1	R
1156	cap5k_1_1	F
1157	cap5k_1_1	R
1158	capBH_1_1	F
1159	cap8H_1_1	R
1160	cap8l_1_1	F
1161	cap8l_1_1	R
1162	cap8J_1_1	F
1163	cap8J_1_1	R
1164	cap8K_1_1	F
1165	cap8K_1_1	R
1166	l-hld_1_1	F
1167	l-hld_1_1	R
1168	l-hysA_1_1	F
1169	l-hysA_1_1	R
1170	l-IgGbg_1_1	F
1171	l-IgGbg_1_1	R
1172	EDIN_1_1	F
1173	EDIN_1_1	R
1174	eta_1_1	F
1175	eta_1_1	R
1176	etb_1_1	F

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SEQ ID NO	Probe name	Direction
1177	etb_1_1	R
1178	hglA_1_1	F
1179	hglA_1_1	R
1180	hglA_2_1	F
1181	hglA_2_1	R
1182	hglB_1_1	F
1183	hglB_1_1	R
1184	hglC_2_1	F
1185	hglC_2_1	R
1186	hla_1_1	F
1187	hla_1_1	R
1188	hlb_1_2	F
1189	hlb_1_2	R
1190	lukF_1_1	F
1191	lukF_1_1	R
1192	lukS_1_1	F
1193	lukS_1_1	R
1194	lukS_2_1	F
1195	lukS_2_1	R
1196	NAG_1_1	F
1197	NAG_1_1	R
1198	sak_1_1	F
1199	sak_1_1	R
1200	sea_1_1	F
1201	sea_1_1	R
1202	seb_1_1	F
1203	seb_1_1	R
1204	sec1_1_1	F
1205	sec1_1_1	R
1206	seg_1_1	F
1207	seg_1_1	R
1208	seh_1_1	F
1209	seh_1_1	R
1210	sel_1_1	F
1211	sel_1_1	R
1212	set15_1_1	F
1213	set15_1_1	R
1214	set6_1_1	F

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SEQ ID NO	Probe name	Direction
1215	set6_1_1	R
1216	set7_1_1	F
1217	set7_1_1	R
1218	set8_1_1	F
1219	set8_1_1	R
1220	sprV8_1_1	F
1221	sprV8_1_1	R
1222	tst_1_1	F
1223	tst_1_1	R
1224	l-sdrC_1_1	F
1225	l-sdrC_1_1	R
1226	l-sdrD_1_1	F
1227	l-sdrD_1_1	R
1228	l-sdrE_1_1	F
1229	l-sdrE_1_1	R
1230	b1169_1_1	F
1231	b1169_1_1	R
1232	envZ_1_1	F
1233	envZ_1_1	R
1234	fliCb_1_1	F
1235	fliCb_1_1	R
1236	nfrB_1_1	F
1237	nfrB_1_1	R
1238	nlpA_1_1	F
1239	nlpA_1_1	R
1240	pilAe_1_1	F
1241	pilAe_1_1	R
1242	yacH_1_1	F
1243	yacH_1_1	R
1244	yagX_1_1	F
1245	yagX_1_1	R
1246	ycdS_1_1	F
1247	ycdS_1_1	R
1248	yciQ_1_1	F
1249	yciQ_1_1	R
1250	ymcA_1_1	F
1251	ymcA_1_1	R
1252	b1202_1_1	F

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SEQ ID NO	Probe name	Direction
1253	b1202_1_1	R
1254	eae_1_1	F
1255	eae_1_1	R
1256	eltB_1_1	F
1257	eltB_1_1	R
1258	escR_1_1	F
1259	escR_1_1	R
1260	escT_1_1	F
1261	escT_1_1	R
1262	escU_1_1	F
1263	escU_1_1	R
1264	espB_1_1	F
1265	espB_1_1	R
1266	fes_1_1	F
1267	fes_1_1	R
1268	fes_2_1	F
1269	fes_2_1	R
1270	fteA_1_1	F
1271	fteA_1_1	R
1272	hlyA_1_1	F
1273	hlyA_1_1	R
1274	hlyB_1_1	F
1275	hlyB_1_1	R
1276	iucA_1_1	F
1277	iucA_1_1	R
1278	iucB_1_1	F
1279	iucB_1_1	R
1280	iucC_1_1	F
1281	iucC_1_1	R
1282	papG_1_1	F
1283	papG_1_1	R
1284	rfbE_1_1	F
1285	rfbE_1_1	R
1286	shuA_1_1	F
1287	shuA_1_1	R
1288	SLTII_1_1	F
1289	SLTII_1_1	R
1290	toxA-LTPA_1_1	F

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SEQ ID NO	Probe name	Direction
1291	toxA-LTPA_1_1	R
1292	VT2vaB_1_1	F
1293	VT2vaB_1_1	R
1294	ardeSE0106_1_1	F
1295	ardeSE0106_1_1	R
1296	ardeSE0107_1_1	F
1297	ardeSE0107_1_1	R
1298	aroiSE0105_1_1	F
1299	aroiSE0105_1_1	R
1300	atIE_1_1	F
1301	atIE_1_1	R
1302	agrB_1_1	F
1303	agrB_1_1	R
1304	agrC_1_1	F
1305	agrC_1_1	R
1306	alphSE1368_1_1	F
1307	alphSE1368_1_1	R
1308	gad_1_1	F
1309	gad_1_1	R
1310	glucSE1191_1_1	F
1311	glucSE1191_1_1	R
1312	hsp10_1_1	F
1313	hsp10_1_1	R
1314	icaA_1_1	F
1315	icaA_1_1	R
1316	icaB_1_1	F
1317	icaB_1_1	R
1318	mvaSSepid_1_1	F
1319	mvaSSepid_1_1	R
1320	nitreSE1972_1_1	F
1321	nitreSE1972_1_1	R
1322	nitreSE1974_1_1	F
1323	nitreSE1974_1_1	R
1324	nitreSE1975_1_1	F
1325	nitreSE1975_1_1	R
1326	oiamtSE1209_1_1	F
1327	oiamtSE1209_1_1	R
1328	ORF1Sepid_1_1	F

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SEQ ID NO	Probe name	Direction
1329	ORF1Sepid_1_1	R
1330	ORF3bSepid_1_1	F
1331	ORF3bSepid_1_1	R
1332	qacR_1_1	F
1333	qacR_1_1	R
1334	sin_1_1	F
1335	sin_1_1	R
1336	ureSE1861_1_1	F
1337	ureSE1861_1_1	R
1338	ureSE1863_1_1	F
1339	ureSE1863_1_1	R
1340	ureSE1864_1_1	F
1341	ureSE1864_1_1	R
1342	ureSE1865_1_1	F
1343	ureSE1865_1_1	R
1344	ureSE1867_1_1	F
1345	ureSE1867_1_1	R
1346	9caD_1_1	F
1347	gcaD_1_1	R
1348	hld_orf5_1_1	F
1349	hld_orf5_1_1	R
1350	icaC_1_1	F
1351	icaC_1_1	R
1352	icaD_1_1	F
1353	icaD_1_1	R
1354	icaR_1_1	F
1355	icaR_1_1	R
1356	psm_beta 1 and2_1_1	F
1357	psm_beta1and2_1_1	R
1358	purR_1_1	F
1359	purR_1_1	R
1360	spoVG_1_1	F
1361	spoVG_1_1	R
1362	yabJ_1_1	F
1363	yabJ_1_1	R
1364	folQShaemolyt_1_1	F
1365	folQShaemolyC_1_1	R
1366	mvaCShaemolyticus_1_1	F

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SEQ ID NO	Probe name	Direction
1367	mvaCShaemolyticus_1_1	R
1368	mvaDShaemolyt_1_1	F
1369	mvaDShaemolyt_1_1	R
1370	mvaK1Shaemolyticus_1_1	F
1371	mvaKiShaemolyticus_1_1	R
1372	mvaSShaemolyticus_1_1	F
1373	mvaSShaemolyticus_1_1	R
1374	RNApolsigm_1_1	F
1375	RNApolsigm_1_1	R
1376	lipShaemolyC1_1	F
1377	lipShaemolyt_1_1	R
1378	agrB2Stalugd_1_1	F
1379	agrB2Stalugd_1_1	R
1380	agrC2Stalugd_1_1	F
1381	agrC2Stalugd_1_1	R
1382	agrCStalugd_1_1	F
1383	agrCStalugd_1_1	R
1384	slamStalugd_1_1	F
1385	slamStalugd_1_1	R
1386	fblStalugd_1_1	F
1387	fblStalugd_1_1	R
1388	slushABCStalugd_1_1	F
1389	slushABCStalugd_1_1	R
1390	RNApolsigmSsapro_1_1	F
1391	RNApolsigmSsapro_1_1	R
1392	RNApolsigmSsapro_1_2	F
1393	RNApolsigmSsapro_1_2	R
1394	msrw1Stwar_1_1	F
1395	msrw1Stwar_1_1	R
1396	nukMStwar_1_1	F
1397	nukMStwar_1_1	R
1398	proDStwar_1_1	F
1399	proDStwar_1_1	R
1400	proMStwar_1_1	F
1401	proMStwar_1_1	R
1402	sigrpoStwar_1_1	F
1403	sigrpoStwar_1_1	R
1404	tnpStwar_1_1	F

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SEQ ID NO	Probe name	Direction
1405	tnpStwar_1_1	R
1406	gehASTwar_1_1	F
1407	gehASTwar_1_1	R
1408	ARG56_1_1	F
1409	ARG56_1_1	R
1410	ASL43f_1_1	F
1411	ASL43f_1_1	R
1412	BGL2_1_1	F
1413	BGL2_1_1	R
1414	CACHS3_1_1	F
1415	CACHS3_1_1	R
1 41 6	CCT8_1_1	F
1417	CCT8_1_1	R
1418	CDC37_1_1	F
1419	CDC37_1_1	R
1420	CEF3_1_1	F
1421	CEF3_1_1	R
1422	CHS1_1_1	F
1423	CHS1_1_1	R
1424	CHS2_1_1	F
1425	CHS2_1_1	R
1426	CHS4_1_1	F
1427	CHS4_1_1	R
1428	CHS5_1_1	F
1429	CHS5_1_1	R
1430	CHT1_1_1	F
1431	CHT1_1_1	R
1432	CHT2_1_1	F
1433	CHT2_1_1	R
1434	CHT4_1_1	F
1435	CHT4_1_1	R
1436	CSA1_1_1	F
1437	CSA1_1_1	R
1438	5triphosphatase_1_1	F
1439	5triphosphatase_1_1	R
1440	AAF1_1_1	F
1441	AAF1_1_1	R
1442	ADH1_1_1	F

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SEQ ID NO	Probe name	Direction
1443	ADH1_1_1	R
1444	ALS1_1_1	F
1445	ALS1_1_1	R
1446	ALS7_1_1	F
1447	ALS7_1_1	R
1448	EDT1_1_1	F
1449	EDT1_1_1	R
1450	ELF_1_1	F
1451	ELF_1_1	R
1452	ESS1_1_1	F
1453	ESS1_1_1	R
1454	FAL1_1_1	F
1455	FAL1_1_1	R
1456	GAP1_1_1	F
1457	GAP1_1_1	R
1458	GNA1_1_1	F
1459	GNA1_1_1	R
1460	GSC1_1_1	F
1461	GSC1_1_1	R
1462	GSL1_1_1	F
1463	GSL1_1_1	R
1464	HIS1_1_1	F
1465	HIS1_1_1	R
1466	HTS1_1_1	F
1467	HTS1_1_1	R
1468	HWP1_2_1	F
1469	HWP1_2_1	R
1470	HYR1_1_1	F
1471	HYR1_1_1	R
1472	INT1a_1_1	F
1473	INT1a_1_1	R
1474	KRE15f_1_1	F
1475	KRE15f_1_1	R
1476	KRE6_1_1	F
1477	KRE6_1_1	R
1478	KRE9_1_1	F
1479	KRE9_1_1	R
1480	MIG1_1_1	F

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SEQ ID NO	Probe name	Direction
1481	MIG1_1_1	R
1482	MLS1_1_1	F
1483	MLS1_1_1	R
1484	MP65_1_1	F
1485	MP65_1_1	R
1486	NDE1_1_1	F
1487	NDE1_1_1	R
1488	PFK2_1_1	F
1489	PFK2_1_1	R
1490	PHR1_1_1	F
1491	PHR1_1_1	R
1492	PHR2_1_1	F
1493	PHR2_1_1	R
1494	PHR3_1_1	F
1495	PHR3_1_1	R
1496	PRA1_1_1	F
1497	PRA1_1_1	R
1498	PRS1_1_1	F
1499	PRS1_1_1	R
1500	RBT1_1_1	F
1501	RBT1_1_1	R
1502	RBT4_1_1	F
1503	RBT4_1_1	R
1504	RHO1_1_1	F
1505	RHO1_1_1	R
1506	RNR1_1_1	F
1507	RNR1_1_1	R
1508	RPB7_1_1	F
1509	RPB7_1_1	R
1510	RPL13_1_1	F
1511	RPL13_1_1	R
1512	RVS167_1_1	F
1513	RVS167_1_1	R
1514	SHA3_1_1	F
1515	SHA3_1_1	R
1516	SKN1_1_1	F
1517	SKN1_1_1	R
1518	SRB1_1_1	F

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SEQ ID NO	Probe name	Direction
1519	SRB1_1_1	R
1520	TCA1_1_1	F
1521	TCA1_1_1	R
1522	TRP1_1_1	F
1523	TRP1_1_1	R
1524	YAE1_1_1	F
1525	YAE1_1_1	R
1526	YRB1_1_1	F
1527	YRB1_1_1	R
1528	YST1exon2_1_1	F
1529	YST1exon2_1_1	R
1530	CCN1_1_1	F
1531	CCN1_1_1	R
1532	CDC28_1_1	F
1533	CDC28_1_1	R
1534	CLN2_1_1	F
1535	CLN2_1_1	R
1536	CPH1_1_1	F
1537	CPH1_1_1	R
1538	CYB1_1_1	F
1539	CYB1_1_1	R
1540	EFG1_1_1	F
1541	EFG1_1_1	R
1542	MNT1_1_1	F
1543	MNT1_1_1	R
1544	RBF1_1_1	F
1545	RBF1_1_1	R
1546	RBF1_2_1	F
1547	RBF1_2_1	R
1548	RIM101_1_1	F
1549	RIM101_1_1	R
1550	RIM8_1_1	F
1551	RIM8_1_1	R
1552	SEC14_1_1	F
1553	SEC14_1_1	R
1554	SEC4_1_1	F
1555	SEC4_1_1	R
1556	TUP1_1_1	F

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SEQ ID NO	Probe name	Direction
1557	TUP1_1_1	R
1558	YPT1_1_1	F
1559	YPT1_1_1	R
1560	ZNF1CZF1_2_1	F
1561	ZNF1CZF1_2_1	R
1562	arcA_1_1	F
1563	arcA_1_1	R
1564	arcC_1_1	F
1565	arcC_1_1	R
1566	bkdA_1_1	F
1567	bkdA_1_1	R
1568	cad_1_1	F
1569	cad_1_1	R
1570	camE1_1_1	F
1571	camE1_1_1	R
1572	csrA_1_1	F
1573	csrA_1_1	R
1574	dacA_1_1	F
1575	dacA_1_1	R
1576	dfr_1_1	F
1577	dfr_1_1	R
1578	dhoD1a_1_1	F
1579	dhoD1a_1_1	R
1580	ABC-eltA_1_1	F
1581	ABC-eltA_1_1	R
1582	agrBfs_1_1	F
1583	agrBfs_1_1	R
1584	agrCfs_1_1	F
1585	agrCfs_1_1	R
1586	dnaE_1_1	F
1587	dnaE_1_1	R
1588	ebsA_1_1	F
1589	ebsA_1_1	R
1590	ebsB_1_1	F
1591	ebsB_1_1	R
1592	eep_1_1	F
1593	eep_1_1	R
1594	efaR_1_1	F

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SEQ ID NO	Probe name	Direction
1595	efaR_1_1	R
1596	gls24_glsB_1_1	F
1597	gls24_glsB_1_1	R
1598	gph_1_1	F
1599	gph_1_1	R
1600	gyrAEf_1_1	F
1601	gyrAEf_1_1	R
1602	metEf_1_1	F
1603	metEf_1_1	R
1604	mntHCb2_1_1	F
1605	mntHCb2_1_1	R
1606	mob2_1_1	F
1607	mob2_1_1	R
1608	mvaD_1_1	F
1609	mvaD_1_1	R
1610	mvaE_1_1	F
1611	mvaE_1_1	R
1612	parC_1_1	F
1613	parC_1_1	R
1614	pcfG_1_1	F
1615	pcfG_1_1	R
1616	phoZ_1_1	F
1617	phoZ_1_1	R
1618	polC_1_1	F
1619	polC_1_1	R
1620	ptb_1_1	F
1621	ptb_1_1	R
1622	recS1_1_1	F
1623	recS1_1_1	R
1624	rpoN_1_1	F
1625	rpoN_1_1	R
1626	tms_1_1	F
1627	tms_1_1	R
1628	tyrDC_1_1	F
1629	tyrDC_1_1	R
1630	tyrS_1_1	F
1631	tyrS_1_1	R
1632	asa1_1_1	F

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SEQ ID NO	Probe name	Direction
1633	asa1_1_1	R
1634	asp1_1_1	F
1635	asp1_1_1	R
1636	cgh_1_1	F
1637	cgh_1_1	R
1638	cylA_1_1	F
1639	cylA_1_1	R
1640	cylB_1_1	F
1641	cylB_1_1	R
1642	cylI_1_1	F
1643	cylI_1_1	R
1644	cylL_cylS_1_1	F
1645	cylL_cylS_1_1	R
1646	cylM_1_1	F
1647	cylM_1_1	R
1648	ace_1_1	F
1649	ace_1_1	R
1650	ef00108_1_1	F
1651	ef00108_1_1	R
1652	ef00109_1_1	F
1653	ef00109_1_1	R
1654	ef0011_1_1	F
1655	ef0011_1_1	R
1656	ef00113_1_1	F
1657	ef00113_1_1	R
1658	ef0012_1_1	F
1659	ef0012_1_1	R
1660	ef0022_1_1	F
1661	ef0022_1_1	R
1662	ef0031_1_1	F
1663	ef0031_1_1	R
1664	ef0032_1_1	F
1665	ef0032_1_1	R
1666	ef0040_1_1	F
1667	ef0040_1_1	R
1668	ef0058_1_1	F
1669	ef0058_1_1	R
1670	enlA_1_1	F

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SEQ ID NO	Probe name	Direction
1671	enIA_1_1	R
1672	esa_1_1	F
1673	esa_1_1	R
1674	esp_1_1	F
1675	esp_1_1	R
1676	gelE_1_1	F
1677	gelE_1_1	R
1678	groEL_1_1	F
1679	groEL_1_1	R
1680	groES_1_1	F
1681	groES_1_1	R
1682	rt1_1_1	F
1683	rt1_1_1	R
1684	sala_1_1	F
1685	sala_1_1	R
1686	salb_1_1	F
1687	salb_1_1	R
1688	sea1_1_1	F
1689	sea1_1_1	R
1690	sep1_1_1	F
1691	sep1_1_1	R
1692	vicK_1_1	F
1693	vicK_1_1	R
1694	yycH_1_1	F
1695	yycH_1_1	R
1696	yycI_1_1	F
1697	yycI_1_1	R
1698	yycJ_1_1	F
1699	yycJ_1_1	R
1700	bglB_1_1	F
1701	bglB_1_1	R
1702	bglR_1_1	F
1703	bglR_1_1	R
1704	bglS_1_1	F
1705	bglS_1_1	R
1706	efmA_1_1	F
1707	efmA_1_1	R
1708	efmB_1_1	F

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SEQ ID NO	Probe name	Direction
1709	efmB_1_1	R
1710	efmC_1_1	F
1711	efmC_1_1	R
1712	mreC_1_1	F
1713	mreC_1_1	R
1714	mreD_1_1	F
1715	mreD_1_1	R
1716	mvaDEfaecium_1_1	F
1717	mvaDEfaecium_1_1	R
1718	mvaEEfaecium_1_1	F
1719	mvaEEfaecium_1_1	R
1720	mvaK1Efaecium_1_1	F
1721	mvaK1Efaecium_1_1	R
1722	mvaK2Efaecium_1_1	F
1723	mvaK2Efaecium_1_1	R
1724	mvaSEfaecium_1_1	F
1725	mvaSEfaecium_1_1	R
1726	orf3_4Efaeciumb_1_1	F
1727	orf3_4Efaeciumb_1_1	R
1728	orf6_7Efaecium_1_1	F
1729	orf6_7Efaecium_1_1	R
1730	orf7_8Efaecium_1_1	F
1731	orf7_8Efaecium_1_1	R
1732	orf9_10Efaecium_1_1	F
1733	orf9_10Efaecium_1_1	R
1734	entA_entl_1_1	F
1735	entA_entl_1_1	R
1736	entD_1_1	F
1737	entD_1_1	R
1738	entR_1_1	F
1739	entR_1_1	R
1740	oep_1_1	F
1741	oep_1_1	R
1742	sagA_1_2	F
1743	sagA_1_2	R
1744	atsA_1_1	F
1745	atsA_1_1	R
1746	atsB_1_1	F

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SEQ ID NO	Probe name	Direction
1747	atsB_1_1	R
1748	budC_1_1	F
1749	budC_1_1	R
1750	citA_1_1	F
1751	citA_1_1	R
1752	citW_1_1	F
1753	citW_1_1	R
1754	citX_1_1	F
1755	citX_1_1	R
1756	dalD_1_1	F
1757	dalD_1_1	R
1758	dalK_1_1	F
1759	dalK_1_1	R
1760	dalT_1_1	F
1761	dalT_1_1	R
1762	acoA_1_1	F
1763	acoA_1_1	R
1764	acoB_1_1	F
1765	acoB_1_1	R
1766	acoC_1_1	F
1767	acoC_1_1	R
1768	ahlK_1_1	F
1769	ahlK_1_1	R
1770	fimK_1_1	F
1771	fimK_1_1	R
1772	glfKPN2_1_1	F
1773	glfKPN2_1_1	R
1774	ltrA_1_1	F
1775	ltrA_1_1	R
1776	mdcC_1_1	F
1777	mdcC_1_1	R
1778	mdcF_1_1	F
1779	mdcF_1_1	R
1780	mdcH_1_1	F
1781	mdcH_1_1	R
1782	mrkA_1_1	F
1783	mrkA_1_1	R
1784	mtrK_1_1	F

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SEQ ID NO	Probe name	Direction
1785	mtrK_1_1	R
1786	nifF_1_1	F
1787	nifF_1_1	R
1788	nifK_1_1	F
1789	nifK_1_1	R
1790	nifN_1_1	F
1791	nifN_1_1	R
1792	tyrP_1_1	F
1793	tyrP_1_1	R
1794	ureA_1_1	F
1795	ureA_1_1	R
1796	wbbO_1_1	F
1797	wbbO_1_1	R
1798	wza_1_1	F
1799	wza_1_1	R
1800	wzb_1_1	F
1801	wzb_1_1	R
1802	wzmKPN2_1_1	F
1803	wzmKPN2_1_1	R
1804	wztKPN2_1_1	F
1805	wztKPN2_1_1	R
1806	yojH_1_1	F
1807	yojH_1_1	R
1808	liac_1_1	F
1809	liac_1_1	R
1810 0	cim_1_1	F
1811	cim_1_1	R
1812	aldA_1_1	F
1813	aldA_1_1	R
1814	aldA_2_1	F
1815	aldA_2_1	R
1816	hemly_1_1	F
1817	hemly_1_1	R
1818	pSL017_1_1	F
1819	pSL017_1_1	R
1820	pSL020_1_1	F
1821	pSL020_1_1	R
1822	rcsA_1_1	F

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SEQ ID NO	Probe name	Direction
1823	rcaA_1_1	R
1824	rmlC_1_1	F
1825	rmlC_1_1	R
1826	rmlD_1_1	F
1827	rmlD_1_1	R
1828	waaG_1_1	F
1829	waaG_1_1	R
1830	wbbD_1_1	F
1831	wbbD_1_1	R
1832	wbbM_1_1	F
1833	wbbM_1_1	R
1834	wbbN_1_1	F
1835	wbbN_1_1	R
1836	wbdA_1_1	F
1837	wbdA_1_1	R
1838	wbdC_1_1	F
1839	wbdC_1_1	R
1840	wztKpn_1_1	F
1841	wztKpn_1_1	R
1842	yibD_1_1	F
1843	yibD_1_1	R
1844	cymA_1_1	F
1845	cymA_1_1	R
1846	cymD_1_1	F
1847	cymD_1_1	R
1848	cymE_1_1	F
1849	cymE_1_1	R
1850	cymH_1_1	F
1851	cymH_1_1	R
1852	cymI_1_1	F
1853	cymI_1_1	R
1854	cymJ_1_1	F
1855	cymJ_1_1	R
1856	ddrA_1_1	F
1857	ddrA_1_1	R
1858	fdt-1_1_1	F
1859	fdt-1_1_1	R
1860	fdt-2_1_1	F

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SEQ ID NO	Probe name	Direction
1861	fdt-2_1_1	R
1862	fdt-3_1_1	F
1863	fdt-3_1_1	R
1864	gatY_1_1	F
1865	gatY_1_1	R
1866	hydH_1_1	F
1867	hydH_1_1	R
1868	masA_1_1	F
1869	masA_1_1	R
1870	nasA_1_1	F
1871	nasA_1_1	R
1872	nasE_1_1	F
1873	nasE_1_1	R
1874	nasF_1_1	F
1875	nasF_1_1	R
1876	pehX_1_1	F
1877	pehX_1_1	R
1878	pelX_1_1	F
1879	pelX_1_1	R
1880	tagH_1_1	F
1881	tagH_1_1	R
1882	tagK_1_1	F
1883	tagK_1_1	R
1884	tagT_1_1	F
1885	tagT_1_1	R
1886	glpR_1_1	F
1887	glpR_1_1	R
1888	lasRb_1_1	F
1889	lasRb_1_1	R
1890	OrfX_1_1	F
1891	OrfX_1_1	R
1892	pa0260_1_1	F
1893	pa0260_1_1	R
1894	pa0572_1_1	F
1895	pa0572_1_1	R
1896	pa0625_1_1	F
1897	pa0625_1_1	R
1898	pa0636_1_1	F

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SEQ ID NO	Probe name	Direction
1899	pa0636_1_1	R
1900	pa1046_1_1	F
1901	pa1046_1_1	R
1902	pa1069_1_1	F
1903	pa1069_1_1	R
1904	pa1846_1_1	F
1905	pa1846_1_1	R
1906	pa3866_1_1	F
1907	pa3866_1_1	R
1908	pa4082_1_1	F
1909	pa4082_1_1	R
1910	pilAp_1_1	F
1911	pilAp_1_1	R
1912	PilAp2_1_1	F
1913	PilAp2_1_1	R
1914	pilC_1_1	F
1915	pilC_1_1	R
1916	PstP_1_1	F
1917	PstP_1_1	R
1918	purK_1_1	F
1919	purK_1_1	R
1920	uvrDII_1_1	F
1921	uvrDII_1_1	R
1922	vsml_1_1	F
1923	vsml_1_1	R
1924	vsmR_1_2	F
1925	vsmR_1_2	R
1926	xcpX_1_1	F
1927	xcpX_1_1	R
1928	aprA_1_1	F
1929	aprA_1_1	R
1930	aprE_1_1	F
1931	aprE_1_1	R
1932	ctx_1_2	F
1933	ctx_1_2	R
1934	algB_1_1	F
1935	algB_1_1	R
1936	algN_1_1	F

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SEQ ID NO	Probe name	Direction
1937	algN_1_1	R
1938	algR_1_1	F
1939	algR_1_1	R
1940	ExoS_1_1	F
1941	ExoS_1_1	R
1942	fpvA_1_1	F
1943	fpvA_1_1	R
1944	lasRa_1_1	F
1945	lasRa_1_1	R
1946	lipA_1_1	F
1947	lipA_1_1	R
1948	lipH_1_1	F
1949	lipH_1_1	R
1950	Orf159_1_2	F
1951	Orf159_1_2	R
1952	Orf252_1_1	F
1953	Orf252_1_1	R
1954	pchG_1_1	F
1955	pchG_1_1	R
1956	PhzA_1_1	F
1957	PhzA_1_1	R
1958	PhzB_1_1	F
1959	PhzB_1_1	R
1960	PLC_1_1	F
1961	PLC_1_1	R
1962	plcN_1_1	F
1963	plcN_1_1	R
1964	plcR_1_1	F
1965	plcR_1_1	R
1966	pvdD_1_1	F
1967	pvdD_1_1	R
1968	pvdF_1_2	F
1969	pvdF_1_2	R
1970	pyocinS1_1_1	F
1971	pyocinS1_1_1	R
1972	pyocinS1im_1_1	F
1973	pyocinS1im_1_1	R
1974	pyocinS2_1_1	F

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SEQ ID NO	Probe name	Direction
1975	pyocinS2_1_1	R
1976	pys2_1_1	F
1977	pys2_1_1	R
1978	pys2_2_1	F
1979	pys2_2_1	R
1980	rbf303_1_1	F
1981	rbf303_1_1	R
1982	rhIA_1_1	F
1983	rhIA_1_1	R
1984	rhIB_1_1	F
1985	rhIB_1_1	R
1986	rhIR_1_1	F
1987	rhIR_1_1	R
1988	TnAP41_1_2	F
1989	TnAP41_1_2	R
1990	toxA_1_1	F
1991	toxA_1_1	R
1992	cap1 EStrpneu_1_1	F
1993	cap1 EStrpneu_1_1	R
1994	cap1 FStrpneu_1_1	F
1995	cap1 FStrpneu_1_1	R
1996	cap1 GStrpneu_1_1	F
1997	cap1 GStrpneu_1_1	R
1998	cap3AStrpneu_1_1	F
1999	cap3AStrpneu_1_1	R
2000	cap3BStrpneu_1_1	F
2001	cap3BStrpneu_1_1	R
2002	celAStrpneu_1_1	F
2003	celAStrpneu_1_1	R
2004	celBStrpneu_1_1	F
2005	celBStrpneu_1_1	R
2006	cglAStrpneu_1_1	F
2007	cglAStrpneu_1_1	R
2008	cglBStrpneu_1_1	F
2009	cglBStrpneu_1_1	R
2010	cglCStrpneu_1_1	F
2011	cglCStrpneu_1_1	R
2012	cglDStrpneu_1_1	F

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SEQ ID NO	Probe name	Direction
2013	cglDStrpneu_1_1	R
2014	cinA_1_1	F
2015	cinA_1_1	R
2016	cps14EStrpneum_1_1	F
2017	cps14EStrpneum_1_1	R
2018	cps14FStrpneum_1_1	F
2019	cps14FStrpneum_1_1	R
2020	cps14GStrpneum_1_1	F
2021	cps14GStrpneum_1_1	R
2022	cps14HStrpneum_1_1	F
2023	cps14HStrpneum_1_1	R
2024	cps19aHStrpneum_1_1	F
2025	cps19aHStrpneum_1_1	R
2026	cps19aIStrpneum_1_1	F
2027	cps19aIStrpneum_1_1	R
2028	cps19aKStrpneum_1_1	F
2029	cps19aKStrpneum_1_1	R
2030	cps19fGStrpneum_1_1	F
2031	cps19fGStrpneum_1_1	R
2032	cps23fGStrpneum_1_1	F
2033	cps23fGStrpneum_1_1	R
2034	dexB_1_1	F
2035	dexB_1_1	R
2036	dinF_1_1	F
2037	dinF_1_1	R
2038	1760Strpneu_1_1	F
2039	1760Strpneu_1_1	R
2040	acyPStrpneu_1_1	F
2041	acyPStrpneu_1_1	R
2042	endAStrpneu_1_1	F
2043	endAStrpneu_1_1	R
2044	exoAStrpneu_1_1	F
2045	exoAStrpneu_1_1	R
2046	exp72_1_1	F
2047	exp72_1_1	R
2048	fnlAStrpneu_1_1	F
2049	fnlAStrpneu_1_1	R
2050	fnlBStrpneu_1_1	F

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SEQ ID NO	Probe name	Direction
2051	fnlBStrpneu_1_1	R
2052	fnlCStrpneu_1_1	F
2053	fnlCStrpneu_1_1	R
2054	gct18Strpneum_1_1	F
2055	gct18Strpneum_1_1	R
2056	hexB1_1_1	F
2057	hexB1_1_1	R
2058	hftsHstrpneu_1_1	F
2059	hftsHstrpneu_1_1	R
2060	immunofrag1Strpneu_1_1	F
2061	immunofrag1Strpneu_1_1	R
2062	immunofrag2Strpneu_2_1	F
2063	immunofrag2Strpneu_2_1	R
2064	immunofrag3Strpneu_2_1	F
2065	immunofrag3Strpneu_2_1	R
2066	kdtBStrpneu_1_1	F
2067	kdtBStrpneu_1_1	R
2068	lysAStrpneu_1_1	F
2069	lysAStrpneu_1_1	R
2070	pcpBStrpneu_1_1	F
2071	pcpBStrpneu_1_1	R
2072	pflCStrpneu_1_1	F
2073	pflCStrpneu_1_1	R
2074	plpA_1_1	F
2075	plpA_1_1	R
2076	prtA1 Strpneu_1_1	F
2077	prtA1 Strpneu_1_1	R
2078	pspC1Strpneu_1_1	F
2079	pspC1Strpneu_1_1	R
2080	pspC2_1_1	F
2081	pspC2_1_1	R
2082	purRStrpneu_1_1	F
2083	purRStrpneu_1_1	R
2084	pyrDAStrpneum_1_1	F
2085	pyrDAStrpneum_1_1	R
2086	SP0828Strpneu_1_1	F
2087	SP0828Strpneu_1_1	R
2088	SP0830Strpneu_1_1	F

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SEQ ID NO	Probe name	Direction
2089	SP0830Strpneu_1_1	R
2090	SP0833Strpneu_1_1	F
2091	SP0833Strpneu_1_1	R
2092	SP0837_38Strpneu_1_1	F
2093	SP0837_38Strpneu_1_1	R
2094	SP0839Strpneu_1_1	F
2095	SP0839Strpneu_1_1	R
2096	ugdStrpneu_1_1	F
2097	ugdStrpneu_1_1	R
2098	uncC_1_1	F
2099	uncC_1_1	R
2100	vicXStrepneu_1_1	F
2101	vicXStrepneu_1_1	R
2102	wchA6bStrpneum_1_1	F
2103	wchA6bStrpneum_1_1	R
2104	wci4Strpneum_1_1	F
2105	wci4Strpneum_1_1	R
2106	wciK4Strpneum_1_1	F
2107	wciK4Strpneum_1_1	R
2108	wciL4Strpneum_1_1	F
2109	wciL4Strpneum_1_1	R
2110	wciN6bStrpneum_1_1	F
2111	wciN6bStrpneum_1_1	R
2112	wciO6bStrpneum_1_1	F
2113	wciO6bStrpneum_1_1	R
2114	wciP6bStrpneum_1_1	F
2115	wciP6bStrpneum_1_1	R
2116	wciY18Strpneum_1_1	F
2117	wciY18Strpneum_1_1	R
2118	wzdbStrpneum_1_1	F
2119	wzdbStrpneum_1_1	R
2120	wze6bStrpneum_1_1	F
2121	wze6bStrpneum_1_1	R
2122	wzy18Strpneum_1_1	F
2123	wzy18Strpneum_1_1	R
2124	wzy4Strpneum_1_1	F
2125	wzy4Strpneum_1_1	R
2126	wzy6bStrpneum_1_1	F

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SEQ ID NO	Probe name	Direction
2127	wzy6bStrpneum_1_1	R
2128	xpt_1_1	F
2129	xpt_1_1	R
2130	igaStrpneu_1_1	F
2131	igaStrpneu_1_1	R
2132	lytA_1_1	F
2133	lytA_1_1	R
2134	nanA_1_1	F
2135	nanA_1_1	R
2136	nanBStrpneu_1_1	F
2137	nanBStrpneu_1_1	R
2138	pcpCStrpneu_1_1	F
2139	pcpCStrpneu_1_1	R
2140	ply_1_1	F
2141	ply_1_1	R
2142	prtAStrpneu_1_1	F
2143	prtAStrpneu_1_1	R
2144	pspA_1_2	F
2145	pspA_1_2	R
2146	SP0834Strpneu_1_1	F
2147	SP0834Strpneu_1_1	R
2148	SP0834Strpneu_1_2	F
2149	SP0834Strpneu_1_2	R
2150	sphtraStrpneu_1_1	F
2151	sphtraStrpneu_1_1	R
2152	wciJStrpneu_1_1	F
2153	wciJStrpneu_1_1	R
2154	wziyStrpneu_1_1	F
2155	wziyStrpneu_1_1	R
2156	wzxStrpneu_1_1	F
2157	wzxStrpneu_1_1	R
2158	cpsA1Strgal_1_1	F
2159	cpsA1Strgal_1_1	R
2160	cpsB1Strgal_1_1	F
2161	cpsB1Strgal_1_1	R
2162	cpsC1Strgal_1_1	F
2163	cpsC1Strgal_1_1	R
2164	cpsD1Strgal_1_1	F

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SEQ ID NO	Probe name	Direction
2165	cpsD1Strgal_1_1	R
2166	cpsE1Strgal_1_1	F
2167	cpsE1Strgal_1_1	R
2168	cpsG1Strgal_1_1	F
2169	cpsG1Strgal_1_1	R
2170	cpsI1Strgal_1_1	F
2171	cpsI1Strgal_1_1	R
2172	cpsJ1Strgal_1_1	F
2173	cpsJ1Strgal_1_1	R
2174	cpsK1Strgal_1_1	F
2175	cpsK1Strgal_1_1	R
2176	cpsM1Strgal_1_1	F
2177	cpsM1Strgal_1_1	R
2178	cpsY1Strgal_1_1	F
2179	cpsY1Strgal_1_1	R
2180	cpsY2Strgal_2_1	F
2181	cpsY2Strgal_2_1	R
2182	cylB1Straga_1_1	F
2183	cylB1Straga_1_1	R
2184	cylE1Straga_1_1	F
2185	cylE1Straga_1_1	R
2186	cylF1Straga_1_1	F
2187	cylF1Straga_1_1	R
2188	cylH1Straga_1_1	F
2189	cylH1Straga_1_1	R
2190	cylI1Straga_1_1	F
2191	cylI1Straga_1_1	R
2192	cylJ1Straga_1_1	F
2193	cylJ1Straga_1_1	R
2194	cylK1Straga_1_1	F
2195	cylK1Straga_1_1	R
2196	0487Straga_1_1	F
2197	0487Straga_1_1	R
2198	0488Straga_1_1	F
2199	0488Straga_1_1	R
2200	0493Straga_1_1	F
2201	0493Straga_1_1	R
2202	0495Straga_1_1	F

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SEQ ID NO	Probe name	Direction
2203	0495Straga_1_1	R
2204	0498Straga_1_1	F
2205	0498Straga_1_1	R
2206	0500Straga_1_1	F
2207	0500Straga_1_1	R
2208	0502Straga_1_1	F
2209	0502Straga_1_1	R
2210	0504Straga_1_1	F
2211	0504Straga_1_1	R
2212	folDStraga_1_1	F
2213	folDStraga_1_1	R
2214	neuA1Strgal_1_1	F
2215	neuA1Strgal_1_1	R
2216	neuB1Strgal_1_1	F
2217	neuB1Strgal_1_1	R
2218	neuC1Strgal_1_1	F
2219	neuC1Strgal_1_1	R
2220	neuD1Strgal_1_1	F
2221	neuD1Strgal_1_1	R
2222	recNStraga_1_1	F
2223	recNStraga_1_1	R
2224	ileSStraga_1_1	F
2225	ileSStraga_1_1	R
2226	CAMPfactor_1_1	F
2227	CAMPfactor_1_1	R
2228	CAMPfactor_2_1	F
2229	CAMPfactor_2_1	R
2230	0499Straga_1_1	F
2231	0499Straga_1_1	R
2232	hylStragal_1_1	F
2233	hylStragal_1_1	R
2234	lipStragal_1_1	F
2235	lipStragal_1_1	R
2236	cyclStrpyog_1_1	F
2237	cyclStrpyog_1_1	R
2238	fah_rph_hlo_Strpyog_1_1	F
2239	fah_rph_hlo_Strpyog_1_1	R
2240	int_1_1	F

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SEQ ID NO	Probe name	Direction
2241	int_1_1	R
2242	int315.5_1_1	F
2243	int315.5_1_1	R
2244	murEStrpyog_1_1	F
2245	murEStrpyog_1_1	R
2246	oppA_1_1	F
2247	oppA_1_1	R
2248	oppCStrpyog_1_1	F
2249	oppCStrpyog_1_1	R
2250	oppD_1_1	F
2251	oppD_1_1	R
2252	SPy0382Strpyog_1_1	F
2253	SPy0382Strpyog_1_1	R
2254	SPy0390Strpyog_1_1	F
2255	SPy0390Strpyog_1_1	R
2256	SpyM3_1351_1_1	F
2257	SpyM3_1351_1_1	R
2258	vicXStrpyog_1_1	F
2259	vicXStrpyog_1_1	R
2260	DNaseIStrpyog_1_1	F
2261	DNaseIStrpyog_1_1	R
2262	fba2Strpyog_1_1	F
2263	fba2Strpyog_1_1	R
2264	fhuAStrpyog_1_1	F
2265	fhuAStrpyog_1_1	R
2266	fhuB1Strpyog_1_1	F
2267	fhuB1Strpyog_1_1	R
2268	fhuDStrpyog_1_1	F
2269	fhuDStrpyog_1_1	R
2270	fhuGStrpyog_1_1	F
2271	fhuGStrpyog_1_1	R
2272	hlyA_1_1	F
2273	hlyA_1_1	R
2274	hlyP_1_1	F
2275	hlyP_1_1	R
2276	hlyp2_1_1	F
2277	hlyp2_1_1	R
2278	oppB_1_1	F

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SEQ ID NO	Probe name	Direction
2279	oppB_1_1	R
2280	ropB_1_1	F
2281	ropB_1_1	R
2282	scpAStrpyog_1_1	F
2283	scpAStrpyog_1_1	R
2284	sloStrpyog_1_1	F
2285	sloStrpyog_1_1	R
2286	smez-4Strpyog_1_1	F
2287	smez-4Strpyog_1_1	R
2288	sof_1_1	F
2289	sof_1_1	R
2290	sof_2_1	F
2291	sof_2_1	R
2292	speA_1_1	F
2293	speA_1_1	R
2294	speB2Strpyog_1_1	F
2295	speB2Strpyog_1_1	R
2296	speCStrpyog_1_1	F
2297	speCStrpyog_1_1	R
2298	speJStrpyog_1_1	F
2299	speJStrpyog_1_1	R
2300	srtBStrpyog_1_1	F
2301	srtBStrpyog_1_1	R
2302	srtCStrpyog_1_1	F
2303	srtCStrpyog_1_1	R
2304	srtEStrpyog_1_1	F
2305	srtEStrpyog_1_1	R
2306	srtFStrpyog_1_1	F
2307	srtFStrpyog_1_1	R
2308	srtGStrpyog_1_1	F
2309	srtGStrpyog_1_1	R
2310	srtIStrpyog_1_1	F
2311	srtIStrpyog_1_1	R
2312	srtKStrpyog_1_1	F
2313	srtKStrpyog_1_1	R
2314	srtRStrpyog_1_1	F
2315	srtRStrpyog_1_1	R
2316	srtTStrpyog_1_1	F

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SEQ ID NO	Probe name	Direction
2317	srtTStrpyog_1_1	R
2318	vicKStrpyog_1_1	F
2319	vicKStrpyog_1_1	R
2320	573Stprmut_1_1	F
2321	573Stprmut_1_1	R
2322	580SSstprmut_1_1	F
2323	580SSstprmut_1_1	R
2324	581_582SSstprmut_1_1	F
2325	581_582SSstprmut_1_1	R
2326	584SSstprmut_1_1	F
2327	584SSstprmut_1_1	R
2328	dltAStrmut_1_1	F
2329	dltAStrmut_1_1	R
2330	dltBStrmut_1_1	F
2331	dltBStrmut_1_1	R
2332	dltCpx1Strmut_1_1	F
2333	dltCpx1Strmut_1_1	R
2334	dltDStrmut_1_1	F
2335	dltDStrmut_1_1	R
2336	lichStrbov_1_1	F
2337	lichStrbov_1_1	R
2338	lytRStprmut_1_1	F
2339	lytRStprmut_1_1	R
2340	lytSStprmut_1_1	F
2341	lytSStprmut_1_1	R
2342	pepQStrmut_1_1	F
2343	pepQStrmut_1_1	R
2344	pflCStrmut_1_1	F
2345	pflCStrmut_1_1	R
2346	recNStprmut_1_1	F
2347	recNStprmut_1_1	R
2348	ytqBStrmut_1_1	F
2349	ytqBStrmut_1_1	R
2350	hlyXStrmut_1_1	F
2351	hlyXStrmut_1_1	R
2352	igaStrmitis_1_1	F
2353	igaStrmitis_1_1	R
2354	igaStrsanguis_1_1	F

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SEQ ID NO	Probe name	Direction
2355	igaStrsanguis_1_1	R
2356	perMStrmut_1_1	F
2357	perMStrmut_1_1	R
2358	atfA_1_1	F
2359	atfA_1_1	R
2360	atfB_1_1	F
2361	atfB_1_1	R
2362	atfC_1_1	F
2363	atfC_1_1	R
2364	ccmPrmi1_1_1	F
2365	ccmPrmi1_1_1	R
2366	cyaPrmi_1_1	F
2367	cyaPrmi_1_1	R
2368	aad_1_1	F
2369	aad_1_1	R
2370	flfB_1_1	F
2371	flfB_1_1	R
2372	flfD_1_1	F
2373	flfD_1_1	R
2374	flfN_1_1	F
2375	flfN_1_1	R
2376	flhD_1_1	F
2377	flhD_1_1	R
2378	floA_1_1	F
2379	floA_1_1	R
2380	ftsK_1_1	F
2381	ftsK_1_1	R
2382	gstB_1_1	F
2383	gstB_1_1	R
2384	hemCPrmi_1_1	F
2385	hemCPrmi_1_1	R
2386	hemDPrmi_1_1	F
2387	hemDPrmi_1_1	R
2388	hev_1_1	F
2389	hev_1_1	R
2390	katA_1_1	F
2391	katA_1_1	R
2392	lpp1_1_1	F

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SEQ ID NO	Probe name	Direction
2393	lpp1_1_1	R
2394	menE_1_1	F
2395	menE_1_1	R
2396	mfd_1_1	F
2397	mfd_1_1	R
2398	nrpA_1_1	F
2399	nrpA_1_1	R
2400	nrpB_1_1	F
2401	nrpB_1_1	R
2402	nrpG_1_1	F
2403	nrpG_1_1	R
2404	nrpS_1_1	F
2405	nrpS_1_1	R
2406	nrpT_1_1	F
2407	nrpT_1_1	R
2408	nrpU_1_1	F
2409	nrpU_1_1	R
2410	pat_1_1	F
2411	pat_1_1	R
2412	pmfA_1_1	F
2413	pmfA_1_1	R
2414	pmfC_1_1	F
2415	pmfC_1_1	R
2416	pmfE_1_1	F
2417	pmfE_1_1	R
2418	ppaA_1_1	F
2419	ppaA_1_1	R
2420	rsbA_1_1	F
2421	rsbA_1_1	R
2422	rsbC_1_1	F
2423	rsbC_1_1	R
2424	speB_1_1	F
2425	speB_1_1	R
2426	stmA_1_1	F
2427	stmA_1_1	R
2428	stmB_1_1	F
2429	stmB_1_1	R
2430	terA_1_1	F

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SEQ ID NO	Probe name	Direction
2431	terA_1_1	R
2432	terD_1_1	F
2433	terD_1_1	R
2434	umoA_1_1	F
2435	umoA_1_1	R
2436	umoB_1_1	F
2437	umoB_1_1	R
2438	umoC_1_1	F
2439	umoC_1_1	R
2440	ureR_1_1	F
2441	ureR_1_1	R
2442	xerC_1_1	F
2443	xerC_1_1	R
2444	ygbA_1_1	F
2445	ygbA_1_1	R
2446	flaA_1_1	F
2447	flaA_1_1	R
2448	flaD_1_1	F
2449	flaD_1_1	R
2450	fliA_1_1	F
2451	fliA_1_1	R
2452	hpmA_1_1	F
2453	hpmA_1_1	R
2454	hpmB_1_1	F
2455	hpmB_1_1	R
2456	lpsPrmi_1_1	F
2457	lpsPrmi_1_1	R
2458	mrpA_1_1	F
2459	mrpA_1_1	R
2460	mrpB_1_1	F
2461	mrpB_1_1	R
2462	mrpC_1_1	F
2463	mrpC_1_1	R
2464	mrpD_1_1	F
2465	mrpD_1_1	R
2466	mrpE_1_1	F
2467	mrpE_1_1	R
2468	mrpF_1_1	F

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SEQ ID NO	Probe name	Direction
2469	mrpF_1_1	R
2470	mrpG_1_1	F
2471	mrpG_1_1	R
2472	mrpH_1_1	F
2473	mrpH_1_1	R
2474	mrpI_1_1	F
2475	mrpI_1_1	R
2476	mrpJ_1_1	F
2477	mrpJ_1_1	R
2478	patA_1_1	F
2479	patA_1_1	R
2480	putA_1_1	F
2481	putA_1_1	R
2482	uca_1_1	F
2483	uca_1_1	R
2484	ureDPrmi_1_1	F
2485	ureDPrmi_1_1	R
2486	ureEPrmi_1_1	F
2487	ureEPrmi_1_1	R
2488	ureFPrmi_1_1	F
2489	ureFPrmi_1_1	R
2490	zapA_1_1	F
2491	zapA_1_1	R
2492	zapB_1_1	F
2493	zapB_1_1	R
2494	zapD_1_1	F
2495	zapD_1_1	R
2496	zapE_1_1	F
2497	zapE_1_1	R
2498	envZPrvu_1_1	F
2499	envZPrvu_1_1	R
2500	frdC_1_1	F
2501	frdC_1_1	R
2502	frdD_1_1	F
2503	frdD_1_1	R
2504	infBPrvu_1_1	F
2505	infBPrvu_1_1	R
2506	lad_1_1	F

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SEQ ID NO	Probe name	Direction
2507	lad_1_1	R
2508	tna2_1_1	F
2509	tna2_1_1	R
2510	end_1_1	F
2511	end_1_1	R
2512	pqrA_1_1	F
2513	pqrA_1_1	R
2514	urg_1_1	F
2515	urg_1_1	R
2516	blaIMP-7_1_1	F
2517	blaIMP-7_1_1	R
2518	mecISepid_1_1	F
2519	mecISepid_1_1	R
2520	blaOXA-10_1_2	F
2521	blaOXA-10_1_2	R
2522	blaB_1_1	F
2523	blaB_1_1	R
2524	ampC_1_1	F
2525	ampC_1_1	R
2526	I-blaR_1_1	F
2527	I-blaR_1_1	R
2528	blaOXA- 32_1_1	F
2529	blaOXA- 32_1_1	R
2530	bla-CTX-M-22_1_1	F
2531	bla-CTX-M-22_1_1	R
2532	pbp2aStrpneu_1_1	F
2533	pbp2aStrpneu_1_1	R
2534	blaSHV-1_1_1	F
2535	blaSHV-1_1_1	R
2536	blaOXA- 2_1_1	F
2537	blaOXA-2_1_12_1_1	R
2538	blaRShaemolyt_1_1	F
2539	blaRShaemolyt_1_1	R
2540	blaIMP-7_1_2	F
2541	blaIMP-7_1_2	R
2542	I-mecR_1_1	F
2543	I-mecR_1_1	R
2544	blaOXY_1_1	F

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SEQ ID NO	Probe name	Direction
2545	blaOXY_1_1	R
2546	dacCStrpyog_1_1	F
2547	dacCStrpyog_1_1	R
2548	femA_1_1	F
2549	femA_1_1	R
2550	mecA_1_1	F
2551	mecA_1_1	R
2552	blaShaemolyt_1_1	F
2553	blaShaemolyt_1_1	R
2554	blavim_1_1	F
2555	blavim_1_1	R
2556	pbp2b_1_1	F
2557	pbp2b_1_1	R
2558	pbp2primeSepid_1_1	F
2559	pbp2primeSepid_1_1	R
2560	pbp2x_1_1	F
2561	pbp2x_1_1	R
2562	pbp3Saureuc_1_1	F
2563	pbp3Saureuc_1_1	R
2564	pbp4_1_1	F
2565	pbp4_1_1	R
2566	pbp5Efaecium_1_1	F
2567	pbp5Efaecium_1_1	R
2568	pbpC_1_1	F
2569	pbpC_1_1	R
2570	l-mecI_1_1	F
2571	l-mecI_1_1	R
2572	pbp1a_1_1	F
2573	pbp1a_1_1	R
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2575	l-blaI_1_1	R
2576	blaTEM-106_1_1	F
2577	blaTEM-106_1_1	R
2578	blaOXY-KLOX_1_1	F
2579	blaOXY-KLOX_1_1	R
2580	ftsWEF_1_1	F
2581	ftsWEF_1_1	R
2582	fmhB_1_1	F

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SEQ ID NO	Probe name	Direction
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2587	femBShaemolyt_1_1	R
2588	blaPER-1_1_1	F
2589	blaPERI-1_1_1	R
2590	bla_FOX-3_1_1	F
2591	bla_FOX-3_1_1	R
2592	blaA_1_1	F
2593	blaA_1_1	R
2594	psrb_1_1	F
2595	Psrb_1_1	R
2596	fmhA_1_1	F
2597	fmhA_1_1	R
2598	mecR1Sepid_1_1	F
2599	mecR1Sepid_1_1	R
2600	blaZ_1_1	F
2601	blaZ_1_1	R
2602	blaOXA-1_1_1	F
2603	blaOXA-1_1_1	R
2604	fox-6_1_1	F
2605	fox-6_1_1	R
2606	blaPrmi_1_1	F
2607	blaPrmi_1_1	R
2608	aacA_aph DStwar_1_1	F
2609	aacA_aphDStwar_1_1	R
2610	aacC1_1_2	F
2611	aacC1_1_2	R
2612	aacC2_1_1	F
2613	aacC2_1_1	R
2614	strB_1_1	F
2615	strB_1_1	R
2616	aadA_1_1	F
2617	aadA_1_1	R
2618	aadB_1_2	F
2619	aadB_1_2	R
2620	aadD_1_1	F

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SEQ ID NO	Probe name	Direction
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2622	aacA4_1_2	F
2623	aacA4_1_2	R
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2625	strA_1_1	R
2626	aph-A3_1_1	F
2627	aph-A3_1_1	R
2628	aacC1_1_1	F
2629	aacC1_1_1	R
2630	aacA4_1_1	F
2631	aacA4_1_1	R
2632	aacA-aphD_1_1	F
2633	aacA-aphD_1_1	R
2634	l-spc_1_1	F
2635	l-spc_1_1	R
2636	aphA3_1_1	F
2637	aphA3_1_1	R
2638	ermC_1_1	F
2639	ermC_1_1	R
2640	linB_1_1	F
2641	linB_1_1	R
2642	satSA_1_1	F
2643	satSA_1_1	R
2644	mdrSA_1_1	F
2645	mdrSA_1_1	R
2646	l-linA_1_1	F
2647	l-linA_1_1	R
2648	ermB_1_2	F
2649	ermB_1_2	R
2650	ermA_1_1	F
2651	ermA_1_1	R
2652	satA_1_1	F
2653	satA_1_1	R
2654	msrA_1_1	F
2655	msrA_1_1	R
2656	mphBM_1_1	F
2657	mphBM_1_1	R
2658	mefA_1_1	F

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SEQ ID NO	Probe name	Direction
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2661	mxr_1_1	R
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2663	dfrStrpneu_1_1	R
2664	dfrA_1_1	F
2665	dfrA_1_1	R
2666	cmIA5_1_1	F
2667	cmIA5_1_1	R
2668	catEfaecium_1_1	F
2669	catEfaecium_1_1	R
2670	cat_1_1	F
2671	cat_1_1	R
2672	tetAJ_1_1	F
2673	tetAJ_1_1	R
2674	tetL_1_1	F
2675	tetL_1_1	R
2676	tetM_1_1	F
2677	tetM_1_1	R
2678	vanH(tn)_1_1	F
2679	vanH(tn)_1_1	R
2680	vanA_1_1	F
2681	vanA_1_1	R
2682	vanHB2_1_1	F
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2684	vanR_1_1	F
2685	vanR_1_1	R
2686	vanRB2_1_1	F
2687	vanRB2_1_1	R
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2689	vanS(tn)_1_1	R
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2691	vanSB2_1_1	R
2692	vanWB2_1_1	F
2693	vanWB2_1_1	R
2694	ddl_1_1	F
2695	ddl_1_1	R
2696	ble_1_1	F

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SEQ ID NO	Probe name	Direction
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2701	vanY(tn)_1_1	R
2702	vanYB2_1_1	F
2703	vanYB2_1_1	R
2704	vanB_1_1	F
2705	vanB_1_1	R
2706	vanZ(tn)_1_1	F
2707	vanZ(tn)_1_1	R
2708	vanC-2_1_1	F
2709	vanC-2_1_1	R
2710	vanX(tn)_1_1	F
2711	vanX(tn)_1_1	R
2712	acrB_1_1	F
2713	acrB_1_1	R
2714	mexB_1_2	F
2715	mexB_1_2	R
2716	l-qacA_1_1	F
2717	l-qacA_1_1	R
2718	sull_1_1	F
2719	sull_1_1	R
2720	sul_1_1	F
2721	sul_1_1	R
2722	cadBStalugd_1_1	F
2723	cadBStalugd_1_1	R
2724	mexA_1_1	F
2725	mexA_1_1	R
2726	acrR_1_1	F
2727	acrR_1_1	R
2728	emeA_1_1	F
2729	emeA_1_1	R
2730	acrA_1_1	F
2731	acrA_1_1	R
2732	rtn_1_1	F
2733	rtn_1_1	R
2734	abcXStrpmut_1_1	F

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SEQ ID NO	Probe name	Direction
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2737	qacEdelta1_1_1	R
2738	elkT-abcA_1_1	F
2739	elkT-abcA_1_1	R
2740	l-cadA_1_1	F
2741	l-cadA_1_1	R
2742	albA_1_1	F
2743	albA_1_1	R
2744	wzm_1_1	F
2745	wzm_1_1	R
2746	msrCb_1_1	F
2747	msrCb_1_1	R
2748	nov_1_1	F
2749	nov_1_1	R
2750	wzt_1_1	F
2751	wzt_1_1	R
2752	wbbI_1_1	F
2753	wbbI_1_1	R
2754	norA23_1_1	F
2755	norA23_1_1	R
2756	mexR_1_1	F
2757	mexR_1_1	R
2758	arr2_1_1	F
2759	arr2_1_1	R
2760	mreA_1_1	F
2761	mreA_1_1	R
2762	l-cadC_1_1	F
2763	l-cadC_1_1	R
2764	uvrA_1_1	F
2765	uvrA_1_1	R
2766	CRD2_1_1	F
2767	CRD2_1_1	R
2768	CDR1_1_1	F
2769	CDR1_1_1	R
2770	CDR1_2_1	F
2771	CDR1_2_1	R
2772	MET3_1_1	F

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SEQ ID NO	Probe name	Direction
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2774	FET3_1_1	F
2775	FET3_1_1	R
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2777	FTR2_1_1	R
2778	MDR1-7_1_1	F
2779	MDR1-7_1_1	R
2780	ERG11_1_1	F
2781	ERG11_1_1	R
2782	SEC20_1_1	F
2783	SEC20_1_1	R
2784	rbcl_1_1	F
2785	rbcl_1_1	R
2786	LDHA(hu)_1_1	F
2787	LDHA(hu)_1_1	R
2788	GAPD(hu)_1_1	F
2789	GAPD(hu)_1_1	R
2790	b-Act(hu)_1_1	F
2791	b-Act(hu)_1_1	R
2792	ARHGDIA(hu)_1_1	F
2793	ARHGDIA(hu)_1_1	R
2794	PGK1(hu)_1_1	F
2795	PGK1(hu)_1_1	R
2796	rbcl_1_2	F
2797	rbcl_1_2	R
2798	16SPa_1_1	F
2799	16SPa_1_1	R
2800	23SEfaecium_2_1	F
2801	23SEfaecium_2_1	R
2802	16SStrepyog_1_1	F
2803	16SStrepyog_1_1	R
2804	16SStrepneu_1_1	F
2805	16SStrepneu_1_1	R
2806	16SStrepagalactiae_1_1	F
2807	16SStrepagalactiae_1_1	R
2808	16SEfaecium_1_1	F
2809	16SEfaecium_1_1	R
2810	16SEfaecium_2_1	F

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SEQ ID NO	Probe name	Direction
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2815	16SKpn_1_1	R
2816	16SSa_3_1	F
2817	16SSa_3_1	R
2818	16SRNAEf_1_1	F
2819	16SRNAEf_1_1	R
2820	16SShominis_1_1	F
2821	16SShominis_1_1	R
2822	16SShaemolyt_1_1	F
2823	16SShaemolyt_1_1	R
2824	23SEfaecium_1_1	F
2825	23SEfaecium_1_1	R
2826	16SrRNAPrmi_1_1	F
2827	16SrRNAPrmi_1_1	R
2828	16SrRNAPrvu1_1_1	F
2829	16SrRNAPrvu1_1_1	R
2830	16SSa_1_1	F
2831	16SSa_1_1	R
2832	16SKlox_1_1	F
2833	16SKlox_1_1	R
2834	p53_1_1	F
2835	p53_1_1	R
2836	0135mihck_1_1	F
2837	0135mihck_1_1	R
2838	FAN_1_1	F
2839	FAN_1_1	R
2840	0270cap_1_1	F
2841	0270cap_1_1	R

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5 <120> DNA microarray for rapid identification of pathogens in blood cultures

<130> 050565ep

10 <160> 2841

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	c c t a a t a a a g a a g g t c a t g g a g a a t t a a t g a t t a a a g g t g c c a a t g t g a t g a a t g g a t a t	1080
55	t t g t a t c c a a c a g a t t t a a c g g g t a c g t t t g a a a a t g g t t a t t t t a a t a c g g g t g a c a t t	1140
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 25 ggtatatctt tcggtatgtt tttacttact attatgccaa cactagtatt tattaatcca 180
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 55 cgaaaacgtc tgaaagttaa atagctgatg atgaatcttc cggttataat aatacacgtg 180

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	tgtttatgtg aatatactga tcatgggtcat tgtggcgtga ttgatgacca tacacatgac	180
55	gttgacaatg ataaatcatt gccactgctt gttaaaacag caatttctca agtggaagct	240

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	ttaaagggtca tgatgatgat tcatcatcta aagaagaacc tgcgaaagag gaagcgccag	240
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	tgaccataac gatggcacia tgagctttgc tgttgagat gtcattggaa aaggatatacc	240
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	gaactcgtga tatttatgtt aatttagaaa atgtgagtta tatggattcg acagggttag	180
40	gtttattcgt aggtacatta aaagcattaa accaaaatga taaagaacta tacatttttag	240
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	tgattcctag aaataatgaa tataaagaga aatatataac aacgattttg aattatgaac	180		
25	ctggtgatat cgttacaatc aaacgtgtga gagataagac cgatttgcta atat	234		
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	tagaaggtac agatttagaa tctaaatcta ttgaagaaat tgttgctaatt ttagacagtg	180		
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	atcatacgat tacaaaagaa atgcaacaaa atttttgaat cattacattt ttttataaaa	180		
	atttcacttt agattcacaa taattactta ttttgtcaat ttatttaatg tcaatatgtt	240		
55	gattaattaa tagtggtgtc taatgtatat aatatttagg tcatcgttat agtcaacaat	300		

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	catgatattg tcaatgatgc gctagatttg ttgcaactac aagatatcag aaatcgtaat	360
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<213> Staphylococcus aureus

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tatctaaaga taatgaagtt gttaaaatag atttatatac ttcagtgccct aacaaacaaa 240
55 atatacaaga tgtaaagaa atgatagaac atcaacaaat cgatgcatta acattttcaa 300

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	gttcgctggc agtacgttat tattttaatg aaggatttgt accaaaattc aagtcgtatt	360
	ttgctattgg agaacaaaca gcacggacca ttaaatacata tcaacaacca gtaacaattg	420
5	cagaaattca aacactcgaa tactaattg aa	452
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	taaccacttg cacctgctcc aaatccataa tattcctcat taaaccagta aaccttatta	180
	tgttctgatt catggccatc taatgcaaaa ttagatattt cgtattgatg gaaaggagat	240
20	tgttctatct tagacatcaa caactgatac atgtcagcac ctaaatcctc attaggaagt	300
	ttaagcaacc cttttctata catattataa aattggggtt taggttcaag tattaagccg	360
	taactcgaaa tatgttgaat atccatatct aaagctagat ctaaactttg ttcaaaatct	420
25	tcaatcgtct gtttcggtaa atgatacatt aaatctaaac tgattgattt aatacctgcg	480
	tttttagcat ttaacaccga agtgtaaata tcttcagtat tgtgcgttct acctaaaaca	540
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30	tctaatagtt ggactttctc tttagttaac tcatcaggat ttgcttcaaa tgtatactcg	660
	cctgtgattg taaacgtatc acgtattgct ttaagtaatc tttccaactg attaatagaa	720
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45	atataattct atgagaatgt ggcaaggggc tagtggtaaa tcaaattata atgggattgt	180
	tagccctgca tatactgtgc tttatccaac acaaaatact agctcattat ttattggata	240
	taagtttaaa acacatagaa tgattcataa atttaaaatt aattcacaag gattaacatc	300
50	agatacatgg aacttaaaat ataaacaatt aaaaaatata aatatagata tacctgtatt	360
	ggaggaacaa gaaaagatag gtgatttctt taaaaaatg gatattattga taagtaacaa	420
55	gaaaatgaaa attgaaatat tagaaaaaga gaaacaatcc tttt	464

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<210> 67
 <211> 533
 <212> DNA
 <213> Staphylococcus aureus

5

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 10 tccggacagt taggtttaat tgatcaaaca gaatatatta gtaaatcagt ttcgtcga 180
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 aatggatacc cattaggggc tattaanaaga ttaactagat atgatatggg tgtattgtcc 300
 15 tctttgtata tttgtttttc tattaanaag gaaatgtcta aagacttcat ggaagcatat 360
 tttgattcga cacttggtg tagagaagtt tctggaattg cagttgaggg tgcaagaaat 420
 cacggattat taaatgtttc tgtgaatgat ttttttacta ttctaattaa atatccaagt 480
 20 ttagaagaac agcaaaaaat aggcaagttc ttcagcaaac tcgaccgaca aat 533

<210> 68
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 <212> DNA
 <213> Staphylococcus aureus

25

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 ggatcaacaa actaggggaaa atgctaatta tcaacgtgaa aacgggtgtg acgaacagca 180
 acatactgaa aattttaacta agaacttgca taatgataaa acaatatcag aagaaaatca 240
 35 tcgtaaaaca gatgatttga ataaagatca actaaaggat gataaaaaag catcgcttaa 300
 taataaaaaat attcaacgtg atacaacaaa aaataacaat gctaattccta gcgatgtaaa 360
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 40 gtcaaaagag gcagataata gtcaagattc aaacgctaata acaatctac cttcacaag 480
 tcgaataaag gaagcaccat cattaaataa gttagatcaa acaagtcaac gagaaattgt 540
 taatgagaca gaaatagaga aagtacaacc acaacaaaat aatcaagcga atgataaaat 600
 45 tactaactac aattttaaca atgaacaaga agtgaaacct caaaaagacg aaaaaacact 660
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<210> 69
 <211> 416
 <212> DNA
 <213> Staphylococcus aureus

55

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	gcatatttcg gggaatgtaa cgcttttcaa acagattggT atgatcatga aacaattgcc	180
	tcagtgaaac atgtaattga gcaatggTtc gaagataata gaaataaatc atttgaaacg	240
10	tatgaagcag cactaaaatt agtagattcT ttggaaaata cgctgctgc aagggaact	300
	attgtcatgg cattgtatcT aatgtttcat gtactgcctt catTTtcagt agcatatgga	360
	gcgacagcga gcggcttatt aaataaacaT ctagagtcTt taaaagcaac aaagcc	416
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	<212> DNA	
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25	aagTtactgc ttttTgatTg tatgtggatg gtgagTtttT tgatcacttc ctgtctccac	180
	aatatggTga ccatacagtt ttaaTtgcat tagctgtaat tgcgattagt tatttagaga	240
	agctagatgt tacaatatTt aaagaagcat tagaaacgTt tggTggTgTt aaacgtcgtt	300
30	tcaatgaaac tacaattgca aatcaagTta ttgtagatga ttatgcacac catccaagag	360
	aaattagTgc tacaattgaa acagcacgaa agaaatatcc	400
35	<210> 71	
	<211> 613	
	<212> DNA	
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	aaacagataa cggcgTaaat agaagTggTt ctgaagatcc aacagtatat agTgcaactt	180
45	caactaaaaa attacataaa gaacctgcga ctttaattaa agcgattgat ggtgatacgg	240
	ttaaattaat gtacaaaggt caaccaatga cattcagact attattggTt gatacacctg	300
	aaacaaagca tcctaaaaaa ggtgtagaga aatatggTcc tgaagcaagt gcattTacga	360
50	aaaaaatggT agaaaatgca aagaaaattg aagTcgagTt tgacaaaggt caaagaactg	420
	ataaatatgg acgtggctTt gcgtatatTt atgctgatgg aaaaatggTa aacgaagctt	480
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acaacgctga ttc 613

5 <210> 72
 <211> 212
 <212> DNA
 <213> Staphylococcus aureus

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 cttctaaatt tccatatgca gcaaattggc gtgcattatc attagacgat actaacggat 180
 15 ttgttaaact tattacactt aaagaagatg at 212

20 <210> 73
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 <212> DNA
 <213> Staphylococcus aureus

25 <400> 73
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 gtttagagac atttctccaa ttgaagattt tactggtaat ttgtcattag agtttgtgga 180
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 35 aaaaatcgac aaaaatggc gtgaaaacta tgatgcaaca attattccaa accgtgggtg 480
 atggttagaa tatgaaacag atgctaaaga tgttgatac gtacgtattg atagaacacg 540
 taaactacca ttaacagtat tgttacgtgc attagggttc tcaagcgacc aagaattgt 600
 40 tgacctttta ggtgacaatg aatatttacg taatacttta gagaaagacg gcaactgaaa 660
 cactgaacaa gcgttattag aaatctatga acgtttacgt ccagggtgaac caccaactgt 720
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45 <210> 74
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 <213> Staphylococcus aureus

50 <400> 74
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 55 ctatgggaca agtattccaa catgtatctt agtattttaa aaatggtgcc aacaagacga 180

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5	atacagttac agtgcgacat tacaagagat tgccgataac gattacaacc taaacatacc	360
	gaggatatgtc gatacatctg aagaagaagc gccaatgat ttagatcaag tocaacaaga	420
	tttgaaaaat atcgacaaaag aaatcgaga aattgaacaa gaaatcaatg catacctgaa	480
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	<211> 468	
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	ttattccaac tgaggagata aaagatgaaa agttgaaaaa ggaaattgaa aactttaagt	180
	tttttgtgca atatggcagt tttaaaggaa tagagaatta tgaaatggt gacatttctt	240
25	ataattctga agctcctatt tattcagcga aatataaact gaaaaatgat gattataatg	300
	ttaaagaatt acgaaaaaga tataatattc caacagaaaa ggcgctaaa ttgttgttga	360
	aaggttcggg ggatttgaaa gggctctcag ttggatataa ggaaattgaa tttatattta	420
30	tagaaaataa aaaagaaaat atatatTTTT cagatggatt aaacttaa	468
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	<211> 512	
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	<213> Staphylococcus aureus	
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	agagttgaga tgaaaaacaa taaaattatt ttattagaca aggtggaaga tcaaaaactt	180
	aaagaaagaa tagaaaactt taaatTTTTT ggacaatatg ccgatttcaa gagtttgaaa	240
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	aaaatgagta ataaagatga aaatgttaag caattaagaa gccgttataa cattcctact	360
	gataaagctc caatattaaa aatgcatatt gatggggact taaaaggcag ttccgttggg	420
50	tataaaaagt tagaaataga cttttcaaaa gaagaaaata gcgaattatc aatagtcgat	480
	tcattaaatt ttcaacctgc caaaaataaa ga	512
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	<211> 502	

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<212> DNA
<213> Staphylococcus aureus

<400> 77

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	aaaaaaatga aaagaaatat ccagtgaat tggatgaataa taggatagtt ttggtaaaag	180
10	atgttaaaga caaaaagtta aaaaatgaaa tagagtcgtt tgaattatct tcacaatatg	240
	gaaactttta tcatcttgat cggaatgaga ttactaatat ttcataataat cctaattgctc	300
	ccaattactc tgcagaatat aaaaatgaaga aaaaatgacag aaacattcaa cagttgaaaa	360
15	agagatttta tctaaaaact agcaagacac caaaattatt gttaaaggga tctggagata	420
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<211> 400
<212> DNA
<213> Staphylococcus aureus

<400> 78

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30	ctaattgagt cattggcata taaatattct aaaggacaat cacatcacga agatttagtt	180
	caagttggta tgggtgggtt aatagggtgcc ataaatagat tcgatatgtc ctttgaacgg	240
	aagtttgaag cttttttagt acctactgta atcgggtgaaa tcaaaagata tctacgagat	300
35	aaaacttgga gtgtacatgt tccgagacgt attaaagaaa ttggggccaag aatcaaaaaa	360
	gtgagcgatg aactaacgc tgaattagag cgttcacctt	400

<210> 79
<211> 529
<212> DNA
<213> Staphylococcus aureus

<400> 79

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	tgttctttgt tgaatttggt gtcagctttt ggtgcttggt catcatttag ctttttagct	120
	tctgctaaaa ggttagcgct ttggcttggg tcatotttta agctttggat gaaaccattg	180
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	aatagggttag cactttgact tgggtcatct ttttaagcttt ggatgaaacc attgcgttgt	360
55	tcttcgttca agttaggcat gttcaagatt tcatagaaag ctttttggtt ttcttttggtt	420

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aaattgttgt cagctttcgg tgcttgagat tcgtttaatt ttttagcttc acctaaaacg 480
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 <210> 80
 <211> 528
 <212> DNA
 <213> Staphylococcus aureus
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	tccggaatgt ctacatatag atcatatcgca gtatttagtc cacctagttg tttagcgggt	240
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25	ggtgtaagaa atggttatac attaggtagc cctattacaa tgggtgttac taatgatgat	240
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	taacaatcga gtcgttgtgc cagagtttcc agtatataaa acttgatgag gtgtttttaa	180
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55	taataatcgg aata	254

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 <211> 716
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 5 <213> Staphylococcus aureus

<400> 85
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 gggacgacaa agacaatcaa gatggtaaga gaccagaaaa agtcagtgtg aatttatttg 180
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 15 ttaaagactt accgaagtat gatgaaggaa agaaaataga atatacagtg accgaagatc 300
 acgtaaaaga ctacacaaca gacatcaacg gtacgacaat aacgaacaag tatacaccag 360
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 25 tggataacaa tgatatgggt aacttgattg tgacaaataa atatacgccg aaaaaaccga 660
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 <211> 581
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 <213> Staphylococcus aureus

<400> 86
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 aaaaatgcag aaaataacac tgagcattca acagtttctg ataagagtga agctgaacaa 180
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 aaaaaaggtg cagcgatcgg tgctggaaca gcagggttgg ctggaggcgc agcaagtaaa 540
 50 agtgcttctg ccgcttcaaa accacatgcc tctaataatg c 581

55 <210> 87
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 <212> DNA
 <213> Staphylococcus aureus

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 10 tttagggtgta tctattgcag tagcacgtgc agcagctgac ttattagggtc aaccacttta 300
 caaatattta ggtggattta atggtaagca gttaccagta ccaatgatga acatcggttaa 360
 tgggtggttct cactcagatg ctccaattgc attccaagaa ttcattgattt tacctgtagg 420
 15 tgctacaacg ttcaaagaat cattacgttg gggtagtgaa attttccaca acttaaaatc 480
 aattttaagc aaacgtgggt tagaaactgc agtaggtgac gaagggtggt 530

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 <211> 560
 <212> DNA
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 25 <400> 88
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 30 caaaaaatta aagaatatga caagtataaa gatttatata aagaatatat gagtaaaaaat 240
 ccaacgtcaa aggtaaaaag agcaaatatt gatcaatata atatcgaaga cctaagagaa 300
 aaagaatata atgatttact aagttctatt aaagatgcgg tagaaacatt taaatcagat 360
 35 gtacaaaaaa tagaatatga aaataaagag ttaaaatctt attcttacga agaagaaaag 420
 aaggctgctt ctagagttga tgatttagca aataaagcgt atagcgttta ttttgcgttt 480
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 40 ttaggtgatg aggacaaacc 560

 45 <210> 89
 <211> 462
 <212> DNA
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 50 <400> 89
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 tgagtattaa tcacaatatc gtagagtaca atgatggtac ttttaaatat caatctagac 180
 caaaatttaa ctcaacacct aaatatatta aattcaaaca tgactataat attttagaat 240
 55 ttaacgatgg tacattcgaa tatgggtgcac gtccacaatt taataaacca gcagcgaaaa 300

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ctgatgcaac tattaaaaaa gaacaaaaat tgattcaagc tcaaaatctt gtgagagaat 360
 5 ttgaaaaaac acatactgtc agtgcacaca gaaaagcaca aaaggcagtc aacttagttt 420
 cgtttgaata caaagtgaag aaaatgggtct tacaagagcg aa 462

 10 <210> 90
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 <212> DNA
 <213> Staphylococcus aureus

 15 <400> 90
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 acactgcgta aagttccgga gataaaaagt acagatgggtc aagttatggc gacaggagaa 180
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 20 ttaactgctg aattatcttt aaatctatth attgatccta caacagtgc gcaaaaagggt 300
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 25 aataaagtag atgggaaatt tagtcatttt gcgtacatga aacctaacaa ccagtcgtta 480
 agctctgtga cagtaactgg tcaagtaact aaaggaaata aaccaggggt taataatcca 540
 30 acagttaagg tatataaaca cattgggttca gacgatttag ctga 584

 35 <210> 91
 <211> 545
 <212> DNA
 <213> Staphylococcus aureus

 40 <400> 91
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 gtggcaggct atattgaaat tccagatgct gatattaaag aaccagtata tccaggacca 240
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 aatcttaaag cagccaaaaa aggtagtatg gtgtacttta aagttggtaa tgaaacacgt 420
 50 aagtataaaa tgacaagtat aagagatggt aagcctacag atgtaggagt tctagatgaa 480
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 55 <210> 92

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<211> 527
<212> DNA
<213> Staphylococcus aureus

5 <400> 92
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10 actttaatga aagttatatt aggttactct agtttcctaaa gcgggaattt taatgttatt 180
aacagcaagg acgaaaaaag caatatcggc gcattgattg aaaatccagg aatatatcct 240
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15 gataaaattg tctcacaact tcatatggat gaatacattc ataaaaaagc taaaacgtat 360
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<213> Staphylococcus aureus

25 <400> 93
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30 atttacaaat gatattgaag ataagggttga tgtaacggct gaactagaaa ttaatttatt 120
tattgatcct aaaactgtac aaactaatgg aaatcaaact ataacttcaa cactaaatga 180
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50 <400> 94
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5	gcgcaacaaa ataagttcaa caaagatcaa caaagcgcct tctatgaaat cttgaacatg	300
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	caaagcacta acgttttagg tgaagctaaa aaattaaacg aatctcaagc accgaaagct	420
10	gacaacaatt tcaacaaaga acaacaaaat gctttctatg aaatcttgaa catgcctaac	480
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25	tgatgtaaca attcataatg ttggaatcaa tccaacacgt tcaggtatta ttgatattgt	180
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	ggatttaaag cagctgaaaa gcctggtagc gaaattcaag acgaaattct ctacaatact	180
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45	ggaatgccaa ttatcgtaa tgggtgta	269
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	<211> 305	
50	<212> DNA	
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55	aggtacacgt atctatgatc cacaacgtga aaaagaaatg cttaacgact taatcgatag	120

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	taacaaagga ccattcaacg ataatactat taagcaatta tttaaagaaa ttttcaaagc	180
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5	acctgaagat acgattgtaa catttgataa tgggggcatt attggagacg gcaataaatc	300
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	gaagttggtg aaaaacaagc tgctgtagac ttaaaagtaa ttttagaata tgggtgaatca	180
20	gcacctaaaa tcttccgtaa agtaactgaa ttagtaaaag aacaagttaa atatattact	240
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	tcaagtatat caagacctg ctattgtcca accaaaaaca gcaaataaca aaacaggcaa	180
35	tgctcaagta agtcaaaaag ttgatactgc acaagtaaat ggtgacactc gtgctaataca	240
	atcagcgact acaaataata cgcagcctgt tgcaaagtca acaagcacta cagcacctaa	300
	aactaacact aatgttacia atgctgggta tagtttagtt gatgatgaag atgataattc	360
40	agaaaatcaa attaattccag aattaattaa atcagctgct aaacctgcag ctcttgaaac	420
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	tcgagttaat aaaaagttga gcggtatcaa tggtagagat actacatata tcaacaatat	180
55	tgtcaccaat aacaacatag cattaaccgg atgtggatta ataattaggt cacctatata	240

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	agcaataata aataactaaaa agcaatgtac caaaaatgct attgataaaa tgaaaatctt	300
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5	tctcatttca attttaaata acgaattaca agccatacat aatacaatcg ggatgaaagc	420
	aattggccaa atattaaata gtaaagttat atatggtgac acactattcg ctgttcccgt	480
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	<211> 637	
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20	taaacgtaac gtgtagcata tgtgattggg aatagaacc acgaatgatc tccaagcact	180
	tctaatecaa aataaacgtt aaaaataaac attaaaactc cgacaacaat agccattaca	240
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	gtaaacaac ttatttgcg accattccat aaatttacgt ttaaatacca atttataaat	600
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45	aatcaggaat tctcacattg gtgaatacag ttatatggga tttggtagtg attttaataa	180
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	gtggattggg gcaaatgtaa ttattatgga tggtttaaca ataaatactg gtgcagtcac	420
	agcagccggc tcagttgtta ctaaaaatgt aggagcatat gaggttggtg gtgggggtcc	480
55	tgcaaaagtg attaagaagc gatttga	507

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5 <210> 103
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 <212> DNA
 <213> Staphylococcus aureus

10 <400> 103
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 15 atttcgacgt attattaatg gtctatttaa gcaattataa aaaagctaatt attgtttatg 300
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 20 gtcattgcagc aaaagaatat tatcaatcta aaggatataa gaaggaagcg aatgttatta 480
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 25 ttgtatatca aggtcaaatt gtaatggaca gaggatatga agagtttatt attgcttcatt 600
 cagcttttaa acaaaatgct ccttcattca taattcgag 639

30 <210> 104
 <211> 380
 <212> DNA
 <213> Staphylococcus aureus

35 <400> 104
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 40 attaatgtct atatgtttgc tttatctagc tttttattat ttttcaccag ataaggaaga 240
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 45 tttcatattt tctgtttcat 380

50 <210> 105
 <211> 500
 <212> DNA
 <213> Staphylococcus aureus

55 <400> 105
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 tttatacaat aataacaatc acgagtgttg tattaggcaa tacgcttaac aatatacgat 180

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	atctgaatgt attttttagg atgactttaa aatataatca gattttgtat attgctctta	420
10	ttcaattttt aggtttgctg ataggactat ttctatatta tttaatccaa aactggattg	480
	tttgttttat taccagtga	500
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15 gcggtgaaag ctgttccgtt caagttgtta ggaataaata caagtttgcc atttcttgca 180
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20 ggtgtttata tagcgcttaa cgtaggtatt attacagcta atcataatat taaaaatttg 360
aagtcacatg caccaggtga agatgtcaaa atagggaatt atagttggat tggaatgaac 420
tcagttatat taccaggagt agaattgggg gaacataca 459

25
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<211> 562
<212> DNA
<213> Staphylococcus aureus

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45 aaatagtttg tctttctcgg ttgttgtgtt ctttataggt attttgtata ccaatacaga 540
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<211> 104
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tgacttagta aaatggatta tcgacacagt gaacaaattc acta 104

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<211> 351
<212> DNA
<213> Staphylococcus aureus

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20 <210> 112
<211> 278
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<213> Staphylococcus aureus

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30 tgataaaaag ctttttggtg atctgttacg tagttgtttt gagttgtttg gtgcttagtt 180
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35 <210> 113
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40 <400> 113
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	aaagtatctt ttagaccttc tataaataca gatgataacg gtaatactga aacaccatat	360
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55	ctagttgtta agatgcaagg cttcattagc tctagaacaa catattcaga cttaaaaaaa	300

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ctcgttttagc cgttgataga aaacatgatg cttttaaaaa ccgaaacgtt acagttaaatt 300
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30 ttataaaaac tttaaaacta gaacatttaa atcaacatat gaaattgatt gggaaaatca 180
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	ggaccatatg atagagattc ttggaacccg gtatatggca atcaactttt catgaaaact	660
20	agaaatgggt ctatgaaagc agcagataac ttccttgatc ctaacaaagc aagttctcta	720
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55	aaagatcaca taagagcaac tcatacatca atttatgaag ttgattggga aaatcatata	180

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	aatattggtg attgcgctga ggtagtcaaa agaacagaag atacaagttg cgataagtgg	180
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	atgtgtatgg atcaaattac tatgtaaact gctatttttc atccaaagat aatgtaggta	180
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55	ttaatatatta gaaatcaagg tgatagtggc aatgatttga gagtaaagtt tgcaactgct	180

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 55 agtaaataa cacctacatc agatggcgaa ctagatattg cccaaggtag tagtatgaga 840

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 45 ttggacaagg tcgtttatta gacaatggca cacaagttgc tctcaagtc agtgaagggtg 180
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 50 <213> Staphylococcus haemolyticus

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	atgtaccaat ggggtgaaca gctgagaaca tagctgaaaa atatgacatc acgcgtgaaa	420
	tgcaagatga gttcgcaaat cattcacaag ctaaagcagc taaagcgacg caagatggta	480
10	aatttaataa tgaaatcatc ggtatgactg acgcagaagg ggaacaaatg acttctgatg	540
	aaggtgttcg cccaaatagt agt	563
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	tcacttacac gtgatacatc acgtttttat caatatttgt tagataacgt tgaaccagat	180
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30	<210> 212 <211> 278 <212> DNA <213> Staphylococcus haemolyticus	
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	aatcaatgtc aagatgactt aagaacattg acggtgagtc acgacaaaat agaaatgttt	180
	cttcgcttag gagaagagaa tggttcagtc gctggcaa ataacaggtgg cggccgtggg	240
40	ggtagtatgc ttatcttagc taaagaattg caaacagc	278
45	<210> 213 <211> 200 <212> DNA <213> Staphylococcus haemolyticus	
50	<400> 213 acgtatatcg tctgaatat tttctaagta gtaaataagac ttatcgatc cagtttggtc	60
	agtagcgtga tcgaattcta aatcatcgaa tcgcttgaag aaactttcat agtcttcaac	120
	tgaaacttct tgacgttcat tcaataaggc tttatgtcct tcaatatcta attgtttttc	180
	atagccttcg actagcgtag	200
55	<210> 214	

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<211> 565
 <212> DNA
 <213> Staphylococcus haemolyticus

5 <400> 214
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 10 tagtcgtagt agtcacgaac aagatagatt atttatagat atagtaaacc acatacaacc 180
 taaacttttt ataaaattta aaagtatatg aatacaaaat gaagatattg aagatttagt 240
 acaagaaact ttaatcagga tttatttagc acttcataca tttgatttta gtacagacgt 300
 15 tccttttgaa cactatttga attgtatcgt acgatcgatg cgaaatgatt tttggagaag 360
 aaaatatatt gagactgata agtacgatag catcattaat gactatgtta ttgactacaa 420
 attgaatcaa tcaagtaa atattgaaga ttttgtatg ataaaagaga aacgagaatt 480
 20 gctagcgagt agtttaacag tattaagtcg attcgagcga aacgtagctg aattactaat 540
 gtctgattat acgcctagt aaatt 565

25 <210> 215
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 <213> Staphylococcus haemolyticus

30 <400> 215
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 aatacagaat tcaacacaag cagaacaagt tgaaaaacag gaacaacctg cttctaataca 180
 35 gacggctaata cactcttcaa aagagtcctc cattaataat caggaaagtc ataacaacaa 240
 gcaacctagt gatgacaaaa cacctaatat caaaccagaa aaaattgaaa aagtagataa 300
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 40 taacaattcg caattaaacc aaaaagaaca tcccaattca tcaaataata aacaacaaaa 420
 gcaacgtcta gatgttaaac cacaaaacga taaccaacaa ttacaatctc gaaatgatgt 480
 aaaaagaaaa ttagataacc agccaattga gcaaaaagat accaagctgc aaagtaacaa 540
 45 taaaagcaaa gacaacacaa cttctgtaaa gtcacacagc caacaacata aaccgcattc 600
 attaaagacc caatccatt taactccagg tcaaa 635

50 <210> 216
 <211> 468
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 <213> Staphylococcus lugdunensis

55 <400> 216
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ccaaggagcg tgacgctaatt ttgaaggcga tagacaaaaa aattgaaaga tttgctagat 120

acttgcagcg tcaaaacaat ctagaccata ttcaattttt gaagatacgc ctaggcttac 180

5 aagtcgcatt aggtaatttt ttcaaaacta ttgttactta tgggtgttgct cttttattcc 240

atacctttct ttacacatta attacacact taacgtattt tttcgttaga cgttttgcg 300

atggtgcaca cgcaaggcca tcattgttgt gccacattca aaatttagtt ttatttgtgg 360

10 cattaccttg gtcaattgtg ctttttcaag tgtcttggac attcatgatt tttgtagcat 420

ttatcgcatt cataattatt atatgttacg caccatcggc aactaaaa 468

15 <210> 217
<211> 450
<212> DNA
<213> Staphylococcus lugdunensis

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gtctttaata tttttgataa ttggatgttt aatattcttt tatttgaaaa taggcttata 180

25 ttccgtttta gcaatctttg gttctgcgct tattatgtat gttagtaatt atatttctgt 240

catccttagt gtaattgctg attatttttc ttttaagttat atagttcaaa taataataat 300

attagtttctg ttactcttaa tatcaataat ttgtgcttat ttcattaggt ttctattaat 360

30 aagctcaaaa aaaacctatc tgtattttcaa caaaatatac atatcagtaa tatctatttt 420

ccttatttta tctttgatca tgctctattt 450

35 <210> 218
<211> 466
<212> DNA
<213> Staphylococcus lugdunensis

<400> 218

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tttacttaag ggattattta gccgttgccg gcataatagt cccttctgcc gtattatttg 120

ttgttttttg cagacaatca attatctttt tacttattat ttgtttaata tacttttatg 180

45 taaaaatagg gttttattct ataatcgcta tattaggctc tgccttaata atgtacataa 240

gtaacttttt ctcaagttca ctcataatat taataggtaa ttttatcaaa tttaggataa 300

tatacgtaat aatttcttta tcatcataca tactgatagg tgttttatgt gcatttatga 360

50 caaaatactt aattaataaa ctcaaaaaaa catacttatt ttttaataaa gtatacataa 420

tcgtcatatc tactttttta acatttacca tcgtatattt ttattt 466

55 <210> 219
<211> 512

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<212> DNA

<213> Staphylococcus lugdunensis

<400> 219

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	caacggttgta tcagcagaat ccaaagata ctaatactca agtttcagga aaactgaata	180
10	attcgaaga aacaaaagca aatgatacag caaccttatt tgcaaaactct aaagtcaatc	240
	aatatattat cgacaatcat cttcagcatt cgccagtagt aaaagatcca cgtatggata	300
	cacttcctaa attagaatat aaaaacggca cttacatggg tgttggttatt cacgaagtgg	360
15	gcgaagacaa tcgctcctta caagtatggg tagatcgcat gtatgaaact tatactagag	420
	catttgta caacattcgtt gataataacg aaatacatct tactgcacct gcagaatatt	480
20	atgtgtgggg agctggctct aaagctaata ca	512

<210> 220

<211> 646

<212> DNA

<213> Staphylococcus lugdunensis

<400> 220

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30	aaacaataaa ctcaagtctga caatgtaaat agcagggcac aagcaataaa tgaaataagc	180
	gacagccatc gtacagtaaa taaagccact gaagcactag acaataactc tacttttaaat	240
	acatccaccg atgtatcacc tgcaacgaaa caagatacaa ctactagcaa tcaaacaact	300
35	caggaaaaca atgatgcaac aacacaaacc aaaacaaatt ataagcaaga tggtaataac	360
	aacgtattat cccaagtagc aaccaatgac aatcagttctt caaatcaacc acgtaacagt	420
	cacctaaata catccacagt aacatacaac aataatcatc aagtaagaag attagcaaaa	480
40	gttgaagcaa caaatacaga taataacggt actcagactt cagacataatc gaataaactc	540
	tcaaatgtaa cagcgacaat tgaagcggca gatacgattt acccacataa agcagaatat	600
45	gtaaatttaa attatcggtt ccaagcccca gatgatgttc aagcag	646

<210> 221

<211> 500

<212> DNA

<213> Staphylococcus lugdunensis

<400> 221

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55	tctttaacta aaatataaat tgagacttta acaataatcg taaaaaggag cgtttacaat	180

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	atgtcaggta tcattgaagc aattactaaa gcagtacaag caggtttaga taaagattgg	240
5	gctacaatgg gcactagcat tgcagaagca cttgctaaag gcattgacgc aatttcaggc	300
	ttatttggtt aatctcaaata ataataaata atactatttta aaataaaaat atttttaaag	360
	gagcgaacat atcatggacg gaatttttga agcaatttct aaagcagtac aagcaggttt	420
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15	<210> 222 <211> 500 <212> DNA <213> Staphylococcus saprophyticus	
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	ctatacatcc aaatgaccaa gaagatttgt gtcaagatgt gctcgtaaga ttatactgtg	180
25	catttaaaaa atttgatttc actgatgaca cacctattga gcattatgta aatcgtgtga	240
	ttaaaaatgt aaaaaatgat tatatccgta aaaaatgcta tggcaaccaa cgacaagaaa	300
	tgctgggtcaa tgaatttata gtcaatgatc aaaatagtaa aacagaacac ccacttgata	360
30	aacatatatt agcttttagag ataggaagtc aattacaaca gggattaatg aaactgacgg	420
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35	<210> 223 <211> 432 <212> DNA <213> Staphylococcus saprophyticus	
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45	ctcgtgaagat tatactgtgc atttaaaaaa tttgatttca ctgatgacac acctattgag	180
	cattatgtaa atcgtgtgat taaaaatgta aaaaatgatt atatccgtaa aaaatgctat	240
	ggcaaccaac gacaagaaat gctgggtcaat gaatttatag tcaatgatca aaatagtaaa	300
50	acagaacacc cacttgataa acatatatta gctttagaga taggaagtca attacaacag	360
	ggattaatga aactgacggc cttagaaaaa agtatcgtaa tctatttact aaatgacttt	420
	aagccgaaag aa	432
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<211> 200
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 <213> Staphylococcus warneri

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 10 gcttcagttg atacgatacc tgggtatagtt ttaaaaaaag cttgaacgcc ccacaaacaa 180
 ccgccagcta catatactat 200

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 <212> DNA
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 aaatccatta ccatcaataa ataatttatt ttgactttct aatgaaaatt ttattagttt 180
 25 acattgaaac aacaaatctt tcaaagaata tctttgcgtt ttttctaaaa atacattgag 240
 tgggtttttc aataagtgat gtaccgtatt atttttaata tcttttaccg aaacactttg 300
 gaccttagta taaaaatagg gtactgaaag agtttctatt tgltttattt ctgaatttat 360
 30 taacttatca ctttaataaat tttcaccgta ctcttctagt ttgttaaaca agctctttcg 420
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 tcttggtaaa attctcactt ctacttctga tgacg 515

35 <210> 226
 <211> 320
 <212> DNA
 <213> Staphylococcus warneri

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 45 gcattcgaac tggcgttgat acgaatcaca atcaatatca aattcttcaa attgataccg 180
 aacatcaacg tattaactg acttctgaag aagatcctca actcatgtat attttagact 240
 acgaagatac aaaccatata ttcatacaaa catcagttaa gaattcgtat ggcacgtcaa 300
 50 gaccataag atacgaaaaa 320

55 <210> 227
 <211> 271
 <212> DNA
 <213> Staphylococcus warneri

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	<400> 227	
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	accgaagatt gataaaggta ataacgtcaa acctgttgaa aagaaagaac gcgcaaattgt	180
	catactacct aacaatgata gacatcaaata taatgataca acgttaggtc actatgctcc	240
10	tggtactttc gttcaagttc aatcaaacga a	271
	<210> 228	
	<211> 500	
	<212> DNA	
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	<400> 228	
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	atcaagaagt gtcatacaaa atatatctag cgcttgagcg ccatcatctt caatatgatg	180
	attcgtttat aaaatatata tcgcgggtca tcaaatcagt taaatgtgat tactatcgac	240
25	ggcattacac tcaacagaag cgatatacga atgtagttaa tgatgctgtg gttgaatatc	300
	aaacgaacct gcttaataga gatcgagttg aaagagaaat attaacaatgt gaagcaatca	360
	aactattgaa cgcggcgtgt gagaaattaa ctaaacaaga acgagaagta tttgaatttt	420
30	atagtaaagg ttataaacca aaagaaatcg cacatttact aggtataaaa gacaaagtag	480
	ttacaatgc gatacaacgt	500
	<210> 229	
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	<212> DNA	
	<213> Staphylococcus warneri	
	<400> 229	
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	atgcattgag ttatcgtgat atatctgaaa tattaaggga acgtgggtga aacgttcac	120
	attcaacggt ctaccgttgg gttcaagaat atgctcccg tttgtatcaa atttgaaga	180
45	aaaaacataa aaaagcgtat tataagtggc gtgttgatga gacatatatc aaaattaaag	240
	gacagtgggtg ttatctgtat cgcgcgattg atgcagatgg acatacatta gatatttgg	300
	tgcgtaagca acgagataat catcagcat atgcgtttat caaacgtctc attaaacaat	360
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	<210> 230	
	<211> 758	
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55	<213> Staphylococcus warneri	

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	aatgcaggat acatcaacta atcaaacaaa cgaaaattct aaacatatta ttgataaaac	180
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10	caattcagaa caatctcttg aagtcgactc aaatgaggca ccagcttcaa atgacaaatc	300
	aactccaacc aaacaagaac ctactaattc aaagcaagat attgatgaaa catctaaacc	360
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15	agaacagtct tctaagaac ctggtgagga taatgctcaa aaagataaac atgtatcaca	480
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	agatgtcaat gtaacacctt caaagtcac atcagaacaa caactatcta caacacaaca	600
20	cattacagct aaagattcta gtgcttcaca agagggtgcca gttcattcac tagattcatc	660
	taaacaagat cacacaacat cgactgagag ccatatcaat ttagataacc tagataaaca	720
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	<211> 562	
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	<213> Candida albicans	
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	<210> 232	
	<211> 524	
	<212> DNA	
	<213> Candida albicans	
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	<211> 230	
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	gtacagccat cttcaactgg tgttgatcct cgtaaataca atgaattatc aacatcaaga	180
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	<211> 633	

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<212> DNA
<213> Candida albicans

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25 <210> 236
<211> 465
<212> DNA
<213> Candida albicans

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<213> Candida albicans

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 caatcgttat caagcccttt accagaacca tttccagtag tttctacacc aacatttacc 300
 55 gttttgattc ctctattctc agaaaaata ctattaagtt tacaagattt aattaaagaa 360

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	caaagctttt caaaactaac gttgctagat tatttgaaac aacttcattc gaaagaatgg	420
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	tttgtacgcg aaaatatgga tgatttgccg tactactgta tcgggttcaa agattcttca	540
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	cggcgccaaa ttagctgtca ttcttggtta agaagagtac ccacaaggcc aattacgaat	420
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<213> Candida albicans

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	tcatcatctg ctccagctac tactccaaat acatctgttc caaccactac tactgaaacc	180
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	acttcatgtt ctaacagtgt ttgtaccgaa agtgaagtta ctactgggtg tattgtcatc	300
	acatctaaag atactattta caccacttac tgtocattga ctgaaactac tccagtttct	360
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	gctgggtcag aatcatccat gcctgccggg gaaacctctc cagctgttcc aaaatcagat	660
	gttccagcta ctgaatcagc tccagttcct gaaatgactc cagctgggtc acaaccatct	720
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	gctcctgctc ctgaaatgac tccagctggg actgaaacta aaccagctgc tccaaaatca	840
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<212> DNA

<213> Candida albicans

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 20 ccacccttaa tacaacatca atggaaagat ccttctcaat tcaattattc tgatgaagat 480
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 25 <210> 264
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 <213> *Candida albicans*

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 gaaattagcc accaccaat caacatatta tcaaagcttt atgagtactt ataccacagc 180
 35 tgaaacccca tcgtctggtt ctattggatt ggggtcaatc agtggaacag taggagaaat 240
 cagaacttat agtatgacta ctatatcaca aggtaatggg gggttatcaa aattcaatca 300
 aaatgggttta gaaatgaaga atttgtcatt tgttaaatta attgggggtt cttttattgc 360
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 <211> 701
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 <213> *Candida albicans*

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 50 caagggtcatt tagaaattct ggctcgttta ccaaattatg gtaatgtaac aggggttatgg 180
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10	atgttgaatg ttacatggta tgaatttggt gataatgccc ataattttcca aacttatggg	660
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35

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	gttcacccac caagaggatg aaagccggca ctgagtataa cattgatgtg ttttaacaagt	660
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25	aaatactaca gaatcctagt cacacatcag aaaaagtc atagtctagta aatccaatag	480
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40	gacaacaatt aactgaattg gggtataaag acagattaga tgatgcatca cttttaagat	180
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	tgagattttc cagagacggc aagttcatcg ccaccggttg caacaaaacc acccaagtgt	240
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	acggaaaact cttggcgaca ggtgcagaag acaagttgat tagaatctgg gatttgagca	420
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	cgctttatca tcgaccaatg ttgaacaagc tttttacact atggcaagac aatcaaagc	180
40	ccaaatgaca aacaatgcc atgccggaaa tgctgccaat gccaaaggga aatctaattgt	240
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	gctggtaata ctataccatc ctcaatccag cagcaaatac caccacagaa tttgtctcca	300
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	<400> 308	
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	ttgctggcat tcaaaaacaa gaattacctt aatatgagca agaattttta acagatatgg	240
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	ctgaagccaa agaagcaatg caagcaggtg ctattttttaa agaagatgca ggacgtggct	180
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	tggggaaggg tctgccaatc aaggagaagt ccaagaagct attaactttg caggcgtaaa	360
	aaaattacca gtcatttttg ttgttgaaaa taatgaatat gcgatttctg toccaattga	420
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	<213> Enterococcus faecalis	
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	ggcaacagca aaccattagt aaatgtccaa tttgatacag aaccagcaag tgactacagc	180
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	aaagaattag gcgctgttaa cgacgtttta gccaaagcaa aaaaagaagt tggaggactt	360
	tctccacgta ttttgacttg gaagttaacc aaaaataaca ataaacttgt ttatacagta	420
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 <213> Enterococcus faecalis

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 tctatgtaga cattgttagt ggcgagccgt tgtttagctc cctggacaaa taogatgctg 180
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 15 attttagtca cggcatgcac cgagtagaag ttcg 274

20 <210> 314
 <211> 564
 <212> DNA
 <213> Enterococcus faecalis

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 gcagccatcg ttgttgatgc tgattctgga gaaattctct ggtcgcagca accagattta 180
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 gaactgttaa aaatgattgc tgtccctct tctaatgttg cgactctcat gttggcaaac 420
 35 ttaatttcag ggaaccagcc tactgacttt gttcatttaa tgaatcaaaa agcggctgaa 480
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 40 ggcctgtatc aaatgcaagg aatt 564

45 <210> 315
 <211> 478
 <212> DNA
 <213> Enterococcus faecalis

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 ggcgaaagtc ttatgaagaa atcgggtcatc cgttgcctaa tagaatgaat attgttgttt 180
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 ctttgcaaat agtagataaa atgtatatca cagaagtaga tttaaatatt gaagatggag 360

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5 atacattctt tccagaattt gatataaatg attttgaagt tttgataggg gaaacacttg 420
 gtgaggaagt gaaatatacg agaacatttt atgtaaggaa aatgaattg agtagatt 478

 10 <210> 316
 <211> 380
 <212> DNA
 <213> Enterococcus faecalis

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 15 taatggttta tatattgaca gtgacaagga agaagtggc attaaaccaa aaggaggctt 180
 cgggtggactg ggcggcgaat atgtcaaacc aacagcgta gccaatgttc gtgcgtttgc 240
 gcaacgtttg aaaccagaaa tcaaaattat tggaacgggc ggtattacat gtggaaaaga 300
 20 tgtttttgag catcttttat gtggtgcgac attagtacaa gttggcacac aattgcatca 360
 agaaggtcca caagtTTTTg 380

 25 <210> 317
 <211> 537
 <212> DNA
 <213> Enterococcus faecalis

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 aaaacataat ttatcagatt tatctcaaac tatcatgtct gacgttgaag gtattgagca 180
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 40 cgatactttg agagaaaact cggaagaatt tcaagaaact attgaattgc agcaagagat 420
 taatagcttt aatctatcta aaaaagttca agacagactt ttcaaaaaaa tggaagagag 480
 45 tgaaaggatt catTTaaagg tagaattaag tactTTTTca gtcattggcct tctctc 537

 50 <210> 318
 <211> 606
 <212> DNA
 <213> Enterococcus faecalis

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 tctggcttat ttaattttct gatgattctg attttatcag ttttatttgg gacgttaagc 120
 55 gaaaccttta ttgtatacgt cgtactgatt tttttacggc ctgtcgcagg tggctggcat 180

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	ttagtcgtat tattttattg gtatgcgcca caaggaacag caattgaacc tgttcagcca	360
	tctgatttaa acgtgctcaa aaagcaaagc cttataaggg tgtgtttact tattttatgt	420
10	agtctgtttg tcaaagaaaa gattgcttca gtaatactct acggtctcgt catccaaggt	480
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	tatggtttcg tttatcaatt acacggagca aacgatttta agtggttttt ttcaacagat	180
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	ccgaattttt tttggttggt tacttttatt gttgattctg ttgttacttt ttgtgttttt	360
	gatttcgcca gagatttcac ctgactttat gcgaggattt gtcacggtaa atagttctaa	420
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	gtcttctgaa aatggatttc ttgggcttaa gaaatttatc catcattgat gataccctca	300
	cagctgttaa acgcgtctat aatcgaacca ttcgtttaaa tcagattcca ttagatgacg	360
55	aaacaacgct ggctttattt agaaaagggg aaacaagtgg cgttttccag tttgaatctg	420

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<211> 407
<212> DNA
<213> Enterococcus faecalis

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acaaaatgtg caagaccagt aaataattgt tgatgctaatt tctggct 407

25
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<211> 607
<212> DNA
<213> Enterococcus faecalis

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tcagcca 607

50
<210> 323
<211> 521
<212> DNA
<213> Enterococcus faecalis

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5	gaaccccgaa aagccgttaa cgttcgtagt tgagcgtaac ggcaaagaag agcaactaac	240
	agtgcacca gaaaaacaaa aagtggaaaa acaaacaatt ggtaaagtcg gcgtttatcc	300
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10	tacgacacag atttttaaaag cactcggctc actattcaca ggcttttagtt taaacaaact	420
	aggtgggcca gtcgatgatgt ttaaattatc ggaagaagca tccaatgctg gagtaagtac	480
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	<213> Enterococcus faecalis	
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	cgaatctggg aagtcttttt agtagagcac ttaaattaca cttggaatga tgtgcacgaa	240
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	catgaggaga aacgccaaac gttaacagac taccctgttg gcacaaaaat tcggattgca	420
	cgtgtcttag acgaaaaaga attactggat tatttagttt ccattgattt aaatattcaa	480
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	aaatatggaa ccacgtgtag aataaacagt taaagggagg aaacaatcat gggctttatt	180
	tgggcattaa ttgtcggcgg ggtcattggg gcaatcgctg gagcaattac taaaaaagga	240
50	tcatcaatgg cattattgca atatcattgc agggtagtt ggttcaaciaa ttggtcaagc	300
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<212> DNA
<213> Enterococcus faecalis

<400> 326

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10 aggaattggc gcaatttgag gaattagtcg aacagggaat cagcagtcga tggctggagc 240
aatTTTTTTA tgattattta cgaaaaaatc tgaaaaagat cgaaccaatt ggtgatttaa 300
aacagttatt tcttgagcta aaacggaaga actataaaat tggattagca acttcagata 360
15 ctttgccagc gactatgttg attatggaat atcttgggtt aacagaaatg tttgatttta 420
ttgcgacagg agatcgttac ttaccgaaac cagatgcgga catgctcaa gccttttgtc 480
agtcatgtca attgaaggcg acagaagtaa tt 512

<210> 327
<211> 643
<212> DNA
<213> Enterococcus faecalis

<400> 327

25 ttatttctgt tgagggcaaa gcggaagcag gtaaatactt gttcttcaca accttaaaag 60
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30 ccattagctt aaaagaagat gatgagttag ttaacgtagt aacgactaat ggcaatcaga 180
agatgattat cggaacacat gcaggatact ctgtcacatt tgatgaaaat actgtacgtg 240
atatgggccc gacagcatca ggtgttcgtg gaatccgtct ccgcgaaaat gattatgtgg 300
35 tcggcgcagc gattctggat gaaaataaag aagtcctagt cattactgaa aatggttatg 360
gtaagcgtac aaagccctct gaatatccag ttaaaggacg tggcggtaaa gggattaaga 420
cagcaaatat cactgagaaa aatgggtccat tagctgggtt aaccacggtc aatgggtgatg 480
40 aagatatctt attgattacg aacaaaggcg tcattatccg ctttaacgtt gattctgttt 540
ctcaaacagg acgcgcaaca ttaggggttc gtttaatgag aatggaagat ggtgccaaag 600
tggtacaat ggctgttgta gaaccagaag aagtggaaga aga 643

<210> 328
<211> 402
<212> DNA
<213> Enterococcus faecalis

<400> 328

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55 cttatgactt tatTTTTATG gatagtgcc aatcaaaata cattgaattt ttacctgaat 180

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gtttacggtt gctgccagtt ggcggcggtt tgatggtgga tgatgtattt caagctggga 240

5 caatttttaga ccctgctgag gaagtaccga aaaaaaatcg agcaattcat cgtaaattaa 300

accaattttt agatgtagtc atggctcacc ctgatttaac ttctacttta gttcctcttg 360

gtgatggagt tattttaatt accaaagaga aagaaacgat ta 402

10 <210> 329
<211> 608
<212> DNA
<213> Enterococcus faecalis

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agccataatg gctacagata tcgctgaggt aattggtggt gccgttgctt tgcaattatt 120

20 atttggtttt ccattattaa ttggtgtggt gataacaacg tttgatgttt tattactgtt 180

gctactgaca aagttaggct ttcgcaaaat cgaagcaatt gtttcttggt taattgcagt 240

catctttttt gtttttgctt atgaagtggc attagcagat ccaaagtgtg gtgaagtatt 300

25 acgagggtttt attccagaca caaaaatagc gacagataaa tccatgttat ttttagcctt 360

ggggatcggt ggagcgacag tcatgcccc aacttatat ttgcattctt ccattgcgca 420

agcacggaaa ttgatcgta acgatgatgt tgagaaagcc aaagcaattc gtttactac 480

30 ttgggattca aatattcaat taactgttgc tttogtcgta aattgtttgt tgttaatttt 540

aggaggagca ttattttatg gaaccaacag tgaattaggt aaatttggtg atttatttga 600

tgctctga 608

35 <210> 330
<211> 450
<212> DNA
<213> Enterococcus faecalis

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atcaacgaga aaccaataat cattccaatc ctgatattga tattgagaaa tctcacttga 120

45 attatgactt agtcaatcct ggttcaatca attatcgga gaaaatcaaa caaatcattg 180

agagccaacg aatcagtaaa cgagcgggta gaaaagacgc agtccttggt aacgaatgga 240

taatcactag tgataccgcc ttttttcaag agaatacaga cacacaagca ttttttaccg 300

50 atgttgctgc atatttctct gatcgctgcg gtgcacaaaa tgctgcctat gccacggtac 360

atttagacga aaccacgcc catatgcact taggaattgt gcctatgtac gaagggcgat 420

tgagcagtaa acaggtgttt agtcggcaaa 450

55 <210> 331

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<211> 360
<212> DNA
<213> *Enterococcus faecalis*

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10 agccgtgatg gaatgaaacg aacagtagaa acttctagct tttatcaagg ttggttgagac 180
aatgtggaaa aagatttatc ccaagttcat gaagcaatta aaacaaaaga cttccctcgt 240
ttaggagaaa tcattgaagc caatgggtta aggatgcatg gaaccacctt aggcgctgtc 300
15 cctccattta cttactggtc ccagggcagc ttacaagcga tggctttagt tcgccaagca 360

<210> 332
<211> 526
<212> DNA
20 <213> *Enterococcus faecalis*
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25 tatacaagtt tcctacgcga cgactataga tgatgctttc ttcataacgg gctaaaattc 120
gttcctgttc tgcttcagtt tggctggaga tttttgctaa taaggctttt ttgcccattt 180
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30 ttttatgttc atcccagact tgggcaaaaag attggatgta ggtttcgttt gacaaaggac 300
catcgaccat aggatacggg tggcctgttg gacgcacaaa gtcatagata tcttgcgta 360
gcatcacatt atcctctttt aaagccaaga tgcgcgggttc actagcaact aacattgcaa 420
35 ccgccccagc tccttgtgta ggctcaccgc cagaatttaa tccatatttt gcaatatctg 480
ctgtacaac caagactttt ttatctggat gtaaggctac gtgatt 526

<210> 333
<211> 512
<212> DNA
40 <213> *Enterococcus faecalis*
<400> 333
45 atccgactat gcgtttactg aagaacaagc tgaagcaatc gttactttac agctataaccg 60
tttaaccaat acggatatta ctgatttaca agaagaagcg aaaacttttag aacaacaaat 120
tgctgagtta ttgaacattt taaacaatga aaaagaacta ttctcagtca tgaaaaaaga 180
50 acttcgcgaa gttaaaaagc aatatggcaa tccgcgctta actcaaattg aagaggaaat 240
ccaagaaatc aagattgaaa cagccgtgtt agttgcgcag gaagacgtgg tcgtaaccgt 300
gacgcacgaa ggctatatca agcggagtag tattcgttct tatacagcat caaaaccaga 360
55 agaaatcggc atgaaagaag gcgacttttt attatatgct ggcgaaagtca atacattaga 420

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tcattctttta ctagtaacaa ataaagggaa tatgatctat cgcgccgtcc atgagttgcc 480

agattttacgc tggaaagaaa ttggcgaaca ta 512

5

<210> 334
<211> 604
<212> DNA
<213> Enterococcus faecalis

10

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acaatgacctg ctcttatatt gagaatgcag aaaaaactga agtcacgaat gataatccgt 120
15 ctgaacactt ggaacattta tttcaatata ttgtgaatga cgataagaca tacatgaaaa 180
aattagtttc tggatcatggc attgtggatc caacaaatcc ttatgaagaa tttaaattaa 240
caaaattaca agcagcaatt caacgaaaaa tcgggtacac attcgatcca aaatcagaac 300
20 gattgcttcc gccaacgtta acagaattag aaaaaggcaa cgcggtttta gcacaccatt 360
taatccaatc attttctcca gaagatgatt taacgccaga aaaaatacat gaaatagggt 420
acaacacggt gatggaattg acaggtggaa agtatgaatt tgtgatcgcc acacatgtcg 480
25 acaaagaaca ttacacaat catattatct ttagttcaac caacttaaaa acaggtaaag 540
cctttcgctg gcaaaaagga accaaaagag tctttgaaca aatttcggat aagattgcag 600
cgaa 604

30

<210> 335
<211> 451
<212> DNA
<213> Enterococcus faecalis

35

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40 atttcatggc agaagaaatt attaaaaatg gtaatgtgga aaaaacagtg actgagtata 180
ttgattttca attaatgtgag gctgaattga aagcagtga aacagcggcg gagtcaaaaag 240
atgttgaaaa aatcgctcag gcattaagaa agatttttga tgaacgttcg aatactggtt 300
45 ggactactgg cggacacaca ggagaagatg taaatgtcta tgcttatggc ccacaagcag 360
aagctttttc aggacaaatt gataatacag accaagcgaa gattattttt ggcttagtag 420
atggcacggg gcaaaaagct gagattaaag a 451

50

<210> 336
<211> 543
<212> DNA
<213> Enterococcus faecalis

55

<400> 336

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5	acacagacac cacaatttga agatcggaaa attatcttac ctggtgataa tgaagcagtt	180
	attccttata tgaagcaaca atattttacca attattgagg aactttatct ctcttatggg	240
	tttcctaaat ttcatattga accaaaaatg gatcaacagc aagctgcaga agtggtgaaa	300
10	aagtttgaag agcaaaaatt agaacaagcc gcagcctttc aacaacaagc tgctgaatcg	360
	cttggttaaac atgaacaaat gaaaaaagaa aaacaacaac aagcgcctgc gtttgatggt	420
	ccaattcggt taggtcggaa tattcccaat gatgaacca ttatgccc atggaaatata	480
15	ctggaagaag aacgtcgtat aacgattgaa ggctttatct ttgataaaga agtgcgtaga	540
	ttg	543
20	<210> 337 <211> 578 <212> DNA <213> Enterococcus faecalis	
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	cgagcaaccg ttgcagttta ttgtatttga tacaatgaa aatcttgata ctgaaaatct	120
	ctggaaatat gttcattgct cagatgaggg cgcggtagca caggaagctg tcagtttagt	180
30	tgcaaccggt caagcacaaa ttttattgaa aggaattatt cagaccaca cattactaaa	240
	agaaatgttg aaaagtggc atcaattaaa aaataaaccc attctttccc atgtagcaat	300
	gggtggagctg cctgcgggaa aaaccttctt gttaaccgat tgtgcgatga atatcgcccc	360
35	cactcaagcg accctcattg aaattgttga aaatgctaaa gaagtcgccc aaaaattggg	420
	actgcaccac ccgaaaattg ctttggttaag cgcagcggaa aatttcaatc ctaaaatgcc	480
40	ttcgtctggt ttagcaaaag aagtcacggc acattttaat aatcaacaag aggctacggt	540
	ttttgggccc ctttcgcttg atttagcgac ctctgaag	578
45	<210> 338 <211> 320 <212> DNA <213> Enterococcus faecalis	
50	<400> 338 aatgcgtgat cagggtgtat gataaaactc ttggaagag gcagaatttt gaaagttgca	60
	tatgcaagag ttcatccat tggcaaaact tggacggca aattcaagag ttaaaaaaat	120
	taggagcgaa aaaaatattt gtagagaaaa aatctggcgc aagtattgaa caacgactaa	180
55	tttttacaga agctatctat tttgtgagag aatccgatat ttttatggta gaagccattg	240
	accgattagg cagaaattac gatgaaatta ttcagacggt taatttattg aaaaataaaa	300

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	atgttcgact cataattaca	320
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	ccacagattt tccgataact agtcgttctt acaccaacca agacgaagaa aataattata	180
15	tgaatcaaatt tccagactat catatatcat tatttgagtc ttttaattgat caaattcatt	240
	tgaattaccg cgatacatat ttgcgaacat tgggtattgtt tttagtagaa tatatagacg	300
	tgaatgggta tttaaagatt tcgttagaag aagcggcaga gaaaaccgaa gcaagcgcca	360
20	ttcaaattgct agatgcatta actttgttac aacagctaga tccagcaggt gtgggggcac	420
	gcaatttaca agaattgtttg atgctacaaa cagaacgaga cgataccgcg cctaacttag	480
	cgtatatattt attggaggaa gagtttgatg ccttagtgag tcgtaaatgg ggcccgttag	540
25	ctaaaaaatt cgggattgaa ttagcagaaa ttcaattgat ttttgattat atacaaacgt	600
	tatcgccagc gccagggaat atttttgatg cgaccgagga attgtatatt cgaccagatt	660
30	taactgtccg aatcaaggaa gatcgaatag tgg	693
35	<210> 340 <211> 210 <212> DNA <213> Enterococcus faecalis	
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	gaatccagac aaggcttctg tttttgattt tgatatggaa gatattaaag tagaaggcta	180
	tgaccacat ccaacgatta aagcgccgat	210
45	<210> 341 <211> 504 <212> DNA <213> Enterococcus faecalis	
50	<400> 341 aacgcacatc tgaaagctac gaaaaaactg tcaaccatat gaaagatgta ttgaatgaaa	60
	tctcttctcg catgcgtaca cattcagttc catggcatac agcaggtaga tattggggac	120
	atatgaactc agaaacatta atgccttctc tattagctta caactttgca atgctatgga	180
55	acgggaacaa cgttgccat gaattctctc cagcaacttc tcaaattggaa gaagaagtag	240

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	gacatgaatt tgctcacttg atgagctaca aaaatggttg gggacacatc gttgctgatg	300
5	gttcttttagc taacttagaa ggcttatggg atgccgtaa cattaaatca ttaccatttg	360
	ctatgaaaga agtaaaacca gaattagttg ctggcgaatc agattgggaa ctattgaaca	420
	tgccaacaaa agaaattatg gacttattag aatcagctga agatgaaatt gatgaaatca	480
10	aagctcattc agctcgttca ggta	504
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	<211> 400	
	<212> DNA	
15	<213> Enterococcus faecalis	
	<400> 342	
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	ggtgtcgatc caactggaga tagcatgcat attggacatt taattccttt tatgatgatg	180
	aaacgattcc aattagcagg tcatcaccca tacattttta ttggtggcgg aactggaaca	240
25	attggtgacc caagtggacg aacaactgaa cgtgttttac aaacgatgga agctgtgcaa	300
	cataatgtgg acagtctttc aaaccaaattg aaaaaattat ttggtaaaga tgctgaggta	360
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	<211> 585	
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40	ccacacctga ttcaaaaggt cgattgaatg ctttcttaca tgatgatcca gtggccacaa	180
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45	tatttttcagg tgcttcatta aattcacgtg gtgaaaacat tacgtatgag ttcgtaaaag	360
	taggaaaacac ggatactggt catgaaatta atggatcaaa agtagctcgt catggaaata	420
	aagtttattc taaaacggat attgatgtag ggacgaatgg gatttcaata agtgactggg	480
50	aagcagttca aggcaaagaa tatattggcg caactgttat ttcaacacca aatagaatta	540
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gtctaaacga gaaagactta aaagctgttg ctgcagcgat taattcagga aaagccaaag 180

10 acgtgaccgc ttcttatgat cttaatttag accaaaacac cgtcacagca atgatgaaaa 240

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ttgtagtgaa aaatgtagaa ggcgattttg aaaatacagc tgttcagctg acaaacgatg 360

15 gtgaaacggg aacaataca gtgattaacc atgtgccagg tagtaatcct tccaaagatg 420

taaaagcaga taaaacggg acagttggca gtgtttctct acatgataaa gatattccgt 480

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20 tcac 544

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<211> 341

<212> DNA

25 <213> Enterococcus faecalis

<400> 345

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aaacattttc ttttccttct tcaatttttt tataatctgc atagcctgaa aagtttaatc 240

35 cagccattcc taatcctttt tcatattattg catcataata aagcggataa tcagcaatcc 300

cagcagcaat tccaattatt gcaaaatgat gatctaaatt t 341

<210> 346

<211> 594

<212> DNA

40 <213> Enterococcus faecalis

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aaacaaagat tttaagtctt ttaattggcc atataaaaaa attttatctc atattgatcc 180

50 agtgaaagaa caactaggga aagatataac catagctcta attgactcgg ggattgatag 240

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gtagatgaa tatgggtcatg gtacacaagt tgctggagta atagacagca ttgctccaag 360

55 agtaaattta aattcttata aggtgatgga tgggacagat ggaaactcta taaatatgct 420

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	taaagctata gttgatgcta caaatgatca agtagatata ataaatgtga gtcttggatc	480
	atataaaaaat atggaaatag acgacgaaag atttactgta gaagcattca gaaaagctgt	540
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	atcaagaata ttcgtactgt ctttgacgaa tatggatttg atgtatcgac atttaaacta	180
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40	gttaaccggg ggaccaatat ttagtctttt ttttacatta accttttttg taaaaattga	240
	cttttttcaa tttttttctt tttttaattt ttcgatattt ttaattactg cagttccttt	300
	taattttaac gggtttatga atgatggata caatatatat aaattagtta ctaaggatta	360
45	tatttttgaa atgtattata ttgtatcaaa tagcttactt aataaatata atcagtcac	420
	tttcttaa atacaactgagg tatgcaaaat aataaaaaaa aataaagaat taccattata	480
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10	tgctaaataa ggaaaatcaa gaaaactatt actctaataa attagaactt gttggtcctt	300
	cttttgaaga gttaagttta gaagaaatgg aagcgattca aggtagtgga gatgttcagg	360
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	gtgaagagca attattagaa gtagatgcta gttatccttt tagatatttc ttacagtatg	300
30	ctcgtttatt tttacttgat ttaaaactcag agttaaatat ttgtacaaaa gaattcatta	360
	ttaattttatt agaaattcta acacaagagc ttattcactt aacaagtaaa acattagtgc	420
	tagatthtga tactthttaa aaaaatgaac ctctaagggt aatgatagt agcaagcgat	480
35	ttatctatta tctaaaaaaa agatttaact ctaaaaaga tataatagct ttttatacat	540
	gctatcctga gttgatgcgt at	562
40		
	<210> 351	
	<211> 590	
	<212> DNA	
	<213> Enterococcus faecalis	
45		
	<400> 351	
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	aagthtttat ctataaagat catgttgtag caacatttaa tgaaaaagtt gaatctttac	120
	ataatgtgaa tgggcatttt tctttcggga ttaaaacgct tatcaccaat agttcgcaac	180
50	cgaatgtgat agaaacggat ttcggaacag caacggcgac tcaacgtttg acgattgaag	240
	gagtgacca caacagagact ggccaaattg agcgagacta tccgtthttt tataaagtag	300
	gcgatttggc tggagagtca aatcaagtac gttggthttt aaatgtgaac ctcaataaat	360
55	ccgatgtcac agaagatatt tcaattgcgg atcgacaagg aagtggtcaa caattaaata	420

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aagagagttt tacatttgat attgtgaatg acaaagaaac taaatatatt tcacttgccg 480
 agtttgagca acaagggttat ggcaaaattg acttcgtaac agataatgac ttttaatttac 540
 5 gtttttatcg ggataaagca cgctttactt cctttatcgt ccgttacact 590

 <210> 352
 <211> 648
 <212> DNA
 <213> Enterococcus faecalis

 <400> 352
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 15 aaagcccaaa accggaaacg aaaacaaaca accaaaaata ccgaagaaaa aatctaatta 120
 tagcaagtat atattcgcat tgtttaccgc acttattcta gtaattgtcg ctactggcgg 180
 ctatatgtgt tatacattaa aacagcaaga agtagaagct caagccaaat atgaaactgc 240
 20 tgtaaaaaat ctcatggctt caatccaaga agagcaagac caaagtggaa tttcaacgaa 300
 aatagatact ataaatgacg gagaaaataa gtgccttatt taccgtccag tttatgaaag 360
 tactgttcct tttaaaaatg caaaccagct cttagacgag cttgctcaaa agcaacaaaa 420
 25 gaagcatcgt gaaaaagaag tgcttacagt tgccagaata aaagcaacag caatatcttc 480
 taaaattggg cagtatagaa ttgaagcaga tagttttatc tgggatcgca gtaaggaaaa 540
 30 ttttaaaaag ccagacagta tttctgagaa agccatttat gtttccgaaa aaactggtaa 600
 agaaatcaca aataaggatt tgattccgga tgaaggaagt ctcttagg 648

 <210> 353
 <211> 520
 <212> DNA
 <213> Enterococcus faecalis

 <400> 353
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 aatcagctga gtataaaatg attcatgaaa ttgatggaac taaaattagt aacggtgaaa 180
 45 atagtaaaga aacaactaca agttcaggaa ctatactggc tgaagaagca atagaaagtt 240
 caaatcaaaa aaattcaaag acaagtgaag tcgaacagga tcttcataaa gatgtatcag 300
 gatctgaatc agtaaaacaa gtagaaactt ctgattctat aaaaaaatct gaagaatcag 360
 50 ctgttaaaac attaaatctg gatgattcac aagagaatac taattcaata actaccaagg 420
 cagaaaatga tgcgctatct acagttaatg atgaaaaagt attaaatgaa agtgatagta 480
 ttatcaaadc aattccttcg gaaacagaga atgtcgataa 520
 55
 <210> 354

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<211> 668
<212> DNA
<213> Enterococcus faecalis

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gtataaataa tccaactgat gcgacagata cacctaaatc gatcgagcag tttgtaaaaa 180
10 gccataaaga tgcttacctt ttatcatgga aagcaggtgg ctttttaccg tctgctagta 240
tttctcaaac gatggtagaa aatgggttta attttactaa tccatcgggg acgtcatttt 300
15 ggcaggcaca caatatgggc ggtgttaaaa cgtcaaaaaa agaagatttt cctgtaactt 360
tagcaacatt cggccaagat tctgttgata tttctggtac aaagccaggg tcaaacgtcg 420
gtgatggcac tgggtggggca tatacctggg ttaaagacta caatgctgga attggttgaa 480
20 aagcagaatt tatggcacac cagacactgt atacaggtgc tatcaataat actgacggat 540
taagtacttt atcagctatt tattcaggag gatgggctac agaccctact tacctcatga 600
agttacaggc cacatataat agcttaggca agcagtttca atgggttgac caagaagcaa 660
25 tacagaaa 668

<210> 355
<211> 517
<212> DNA
<213> Enterococcus faecalis

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35 atacgttaaa atatgaatag atatagatag taattatatt atctataaat agtagagtat 120
aacgatcttt tattttttga ttttctataa attttaagta gtaagaaaat ctttttcgtt 180
caaacttttc tataatctct aaatttttaa tttgaacaga attagttgaa ataagcatat 240
40 aaaaatttaa tagtaattgc tccttatcag attttagacg tactctttca attatattca 300
tgatatattc atcgatggta gagcttttat cagcaatttt ttctaattca gagttttatta 360
tatccaaatt atacacaatc actgcctcat ataaatcatg ttttgtttta aaaaagctat 420
45 atacggtagt agtgctggtt ttagcttcat tagcaatatc taaaagtttt gttttttcat 480
aaccaaattt agaaaagtgt ttcattgcgg taaatat 517

<210> 356
<211> 380
<212> DNA
<213> Enterococcus faecalis

50 <400> 356
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	aggctaaatt cgttggaatt tgtggatgtt tggttagaca aagaaacaca aaaaatcaca	120
	ctaaaacgct gtttttatga tacgtctttc aagaaacaaa cactaaaaga gttagaacga	180
5	gtatatattcc aattaaaaga aataatcaac gtgcaaataa acaagcggtc tttaaatcgc	240
	aatgacatac gtaatgtacg agaactagag gaaaaacaac aagaaataaa acgattcatg	300
	ttagacgttt tagaagatgc ttattggaaa gaattagcaa atatgccaga agaccaacga	360
10	cacttagacg attgggattt	380
	<210> 357	
	<211> 320	
15	<212> DNA	
	<213> Enterococcus faecalis	
	<400> 357	
	aaagtactac cttttattgc cttagtccgc ttgttattgt tgtcagggtg tggaacagat	60
20	atgaaaaaga tattgactgc cgatgggtgg aaatggaaaag tggaagaaac acgtgcaact	120
	tacacttttt ttgatgacgg taaattttca gctaattgact cagaggatag tgttagtggg	180
	acatacaatt atgatgaaaa aaataaaaaa ataacctttg acattactag cagaaactct	240
25	ttcattatgg aaaaagtaga atacaaagat aacaagatta caggggaaat tggcgaaaaa	300
	caaagaacac ttataaaaca	320
	<210> 358	
30	<211> 503	
	<212> DNA	
	<213> Enterococcus faecalis	
	<400> 358	
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	aaacgatcaa cgtataccag ctgatattgt taggcacgtg gatggcgata ccacagtatt	120
	aaaaattgac ggaaaagaac aaaaagttcg gtttttatta attgacacac ccgagactgt	180
40	gaaaccgaaa acaaaagttc agccgttcgg attggaagct agcaaacgca caaaagagct	240
	tttgtctact gtttcagaaa ttacgtttga atatgataag ggcgataaaa cagatcgтта	300
	cggacgagcg ttgggctaca tattcgtaga tggaacatta ctacaaaaaa cgcttgtaag	360
45	tgaaggatta gctcgtgttg cctatgtaaa agagcctaca actaagtatt tggcagaact	420
	agagcaagcc caagaacagg ctaaaaatga gtcactcgga atctggagca taccaggtta	480
50	tgtgacacaa cgggggttta gta	503
	<210> 359	
	<211> 220	
	<212> DNA	
55	<213> Enterococcus faecalis	
	<400> 359	

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	tgatgaaaat ttaaaagaag aagcagaaca attatattgat gatttagggg taaatatgac	60
	aagtgcattt acgattttct taaaacagtc tattaatgag caagcaattc cttttatgat	120
5	taataaggga aacaaagaga ctctacaagc attaaaagac attaaagaag gaaatgttca	180
	tggtggattt tcttccgtgg aggatttaat ggaggattta	220
10	<210> 360 <211> 380 <212> DNA <213> Enterococcus faecalis	
15	<400> 360 tcaaatacac gtaagccttc tttcgtgctt tcaaccacaa tagattgctc tttatcagcc	60
	aacagccaat ggagagggga taacggaagt tcatcactaa aattaatatt tactaaatta	120
	agattcttca ataatttttt tgcttcatct acagtagagc attggcccaa taccoaagga	180
20	ataaactcaa atggagaaac attttctttt ccttcttcaa tttttttata atctgcatag	240
	cctgaaaagt ttaateccagc cattcctaatt cctttttcat ttattgcatc ataataaagc	300
	ggataatcag caatcccagc agcaattcca attattgcaa aatgatgatc taaatttcca	360
25	acttctcgaa atgaaaactt	380
30	<210> 361 <211> 511 <212> DNA <213> Enterococcus faecalis	
35	<400> 361 cattattttc attaggggat attagagata ttcttctcct tataaattat ttttttacgg	60
	gaaagattga agacttattt cataagccgt tacatgatta tgagaaaaaa ttttcagaag	120
	atatccaaat agaacggata gatattgtat tatctcaaaa ttatgatcca gaaatttatt	180
	tatttttata tgaaaataaa atttttagaat atgttgtaaa tggtaatgta caagaattaa	240
40	gtaatatgat atttaaaacta agtaatggtg ttgttctctg ggtagtgagg gataacgtac	300
	gttctgaaaa gaattattca atagttgtat ttgagaagtt agcacaagca gctataaata	360
	tgggaatgga cttaataaat gcatatcaga gtogagatag ttttataagg aaaaatgaac	420
45	tatgtataaa tttaaaagaa gtattaaaag ttagagatac tgctatagta ttttatacct	480
	ctgaaatagg aaaagctaaa gtaaggaatc t	511
50	<210> 362 <211> 526 <212> DNA <213> Enterococcus faecalis	
55	<400> 362 ttgcgatttc tgtttagtag accattattt ttgtaatagg actttatggt agtaaaataa	60

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	aaaaataaat cacaattaag gttctggttg ttattaatct atctcatgaa gcattagatg	120
	aattagttct agaagtacct gttgtactag ttaaaaatac tgtaaataca aattttttgt	180
5	ttaaaaagaat cattaagttg gtgcctaact ataaaatcaa attgactaaa atccaataac	240
	attgggggat actctgtaaa tcgtgtgtcg cagtacgtta gtcttgtaat aaatagatct	300
	taattaggag gggtttctat gaaaaatatt ttactttcta ttctaggggt attatctatc	360
10	gttgtttctt tggcgttttc ttcttattct gtcaacgcag cttctaata gaaggtcgtgg	420
	ccactgggca aaccatatgc gggaagatat gaagaaggac aacaattcgg gaacactgca	480
	tttaaccgag gaggtactta ttccatgat gggtttgact ttgggt	526
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	<210> 363	
	<211> 505	
	<212> DNA	
	<213> Enterococcus faecalis	
20		
	<400> 363	
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	gatttagtga aaaaagtgtg gcaagacaaa attgagctgc atagtattgt gccaatggg	120
25	acagaccctc acgaatatga accgttacca gaagacattg cgaaagcttc tgaagcggac	180
	attttattct ttaacggctt gaacttagaa acaggcggaa atggctggtt taacaaatta	240
	atgaaaacgg ccaaaaaagt tgagaataaa gattactttt ctacaagcaa aaatgttacg	300
30	ccacaatatt taacaagtgc cgtcaagaa caaacagaag atccgcatgc ttgggttagac	360
	attgaaaatg gcatcaata tgtagaaaac attcgtgacg tgttagtaga aaaagatcca	420
	aaaaataaag atttctatac agaaaacgcg aaaaattata ccgaaaaact tagcaaacta	480
35	catgaggaag ccaaagctaa atttg	505
	<210> 364	
	<211> 557	
	<212> DNA	
	<213> Enterococcus faecalis	
40		
	<400> 364	
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45	cgggatatac gaagaattat aatttctcgg atttacaatt caaccctaaa gcaataactg	120
	gtgatgtgtt acagggaaat acaattgatt ttgaggttta tgggaaacat aatattgcag	180
	cttcaactgc aaactgggaa attcgtcttc aattagatga acgattggcc cagtatgttg	240
50	aaaaaattca agttgatccg aagaagggcg taggaaatag tagacgaact tttgtaagaa	300
	ttaatgattc gcttggcaga cctacaaaca tttggaaggt taattacatt cgagcaaatg	360
	atggactatt tgctggggca gaaacaactg atacacaaac tgctcctaac ggtgtgatta	420
55	catttgaaaa aaatttagat gaaattttta aagaatttgg tgcagataat cttaaaagcg	480

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accgtttaat gtatcgtatc tatttggtaa gtcatacaaga tgacgataaa attgtacctg 540

gaatagaaag cactggg 557

5

<210> 365
<211> 523
<212> DNA
<213> Enterococcus faecalis

10

<400> 365
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agaacaagtt tattcagaaa gtgaagtttc aacagtttta tcgaagttgg aaaaggaggc 120
aatttctgag gcagctgctg aacaatatac ggttgtagat cgaaaagaag acgcgtgggg 180
gatgaagcat ctttaagttag aaaagcaaac ggaaggcggt actgttgatt cagataatgt 240
gattattcat ttagataaaa acggtgcagt aacaagtgtt acaggaaatc cagttgatca 300
agttgtgaaa attcaatcgg ttgatgcaat cgggtgaagaa ggagttaaaa aaattattgc 360
ttctgataat ccggaataa aagatcttgt ctttttagct attgacaaac gtgtaaataa 420
tgaagggcaa ttatcttata aagtcagagt aacttcttca ccaactgggtg accccgtatc 480
attggtttat aaagtgaacg ctacagatgg aacaattatg gaa 523

20

25

30

<210> 366
<211> 400
<212> DNA
<213> Enterococcus faecalis

<400> 366
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caacgtctga ttttgatcgt gaaaaattac aagaacgttt agctaaatta gctggcgggg 120
ttgctgtcgt taaagtcggg gctgcaactg aaacagaatt aaaagaatta aaattacgaa 180
ttgaagatgc attaaacgca acacgtgccg ctgtagaaga aggcattggt tctgggtggtg 240
gtaccgcact tgcattgta attggtaaag tcgctgcgct agaagctgaa ggcgatgtgg 300
caacagggat caagattgtc gttcgtgcat tagaagaacc aatccgtcaa atcgtgaaa 360
atgctggtta tgaaggatca gtgattgttg acaaactaaa 400

35

40

45

50

<210> 367
<211> 264
<212> DNA
<213> Enterococcus faecalis

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gcatccgttg cacaagaaaa accacaaaca ggtgaagtta tcgcagtagg tgaaggctcg 120
gtgcttgaat atggcacaaa agttccgatg gaagtaaaaa ttggtgacac agtaattgtt 180

55

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gaaaaaatatt caggaacaga agtgaaatac gaaggcgtag aatacttaat tgtatcagcc 240
 aaagacatta ttgccactgt tgaa 264
 5
 <210> 368
 <211> 505
 <212> DNA
 <213> Enterococcus faecalis
 10
 <400> 368
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 tttcagatga tggttctact gatcatacgt tggaaatttt gagaacgtat gcagcgaatt 120
 15 atccccaat tcaattgtta caaggtccag ggcaaggagt gattgctaatt tttgcatttg 180
 cgcttacgca tacgaaaggc gaagtgatat ttttagcaga tcaagatgac gtttggttgc 240
 caaataaagt aacaacagt acagaatatt ttgaaacgca ccctgacatc caagtggtta 300
 20 ttagtgactt gaaaattggt gatgcggatt tacaagttac caatccctct tattttaagt 360
 ttcgaaaagt caaaccaggg ttttgccgaa atgcgataaa aagtggctat attggggcag 420
 gtatggcctt tcgtcaagag atgaaaaacg tcattttacc cattccgcca gaagttccta 480
 25 tgcattgatat gtggattggc ttatt 505
 <210> 369
 <211> 688
 <212> DNA
 <213> Enterococcus faecalis
 30
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 35 gcagatgaat acgatacaaa gattcaacaa caagatcaaa aaattaatgc gttaactagc 120
 caaatgtcag atgcagaagc aaaagttgcc gcgattgaaa atgatatggt tgaaacggcc 180
 aaacaaatcg atacattaac agctaaaaag aacaagctat catcagaagt atctaaatta 240
 40 tatagtgaat tttctgattt gaatgtccgt attcaaaaac gtgaagtaca aatgacaaaa 300
 caagcagcgc atgtccaagt gaatgggtcaa agtgattcaa ttattgatgc tgtcttagat 360
 45 gcagattcag tagcagatgc aattgggtcgc gttcaagcgg tctcaacaat gatgagcgcc 420
 aataatgaat tactagaaca acaaaaagaa gacaaagcga ctggtgaaaa gaaaacaaaag 480
 aatgttgaaa aacaaattgc tgaattagaa gcagcaacaa aagaattaaa tgataaaaca 540
 50 gaatcattaa aaacattgaa gattcaacaa gaagtggcta aaaatgattt agaagcacia 600
 cgttctgaag aacaagggaa aaaagacggc ttcattaaac agaaaaaaga agcggaaaaa 660
 cgtttagcag aagaacaagc acgtcaac 688
 55
 <210> 370

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<211> 500
<212> DNA
<213> Enterococcus faecalis

5 <400> 370
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aaagcagctg ctgaagcaga gcaagcacgc ttagctgctg aacaaaaagc tgcagctgaa 120
10 aaagccaaac aagctgctgc aaaaccagct aaagctgaag tgaaagcaga agcaccagtt 180
gcctcttcat caacaacaga agcacaagca ccagcaagct caagctcagc aactgaatca 240
agcacgcaac aaacaactga aacaactaca ccaagtacag ataatagtgc aacagaaaat 300
15 actggctctt cttcatcaga acaaccagta caacctacaa caccaagcga taatggaaat 360
aatgggtggc aaactgggtg tggaacagtt acaccaacac cagaaccaac accagcgcct 420
tctgctgac caacaatcaa tgcattgaac gttctacgtc aatcattagg ttacgtcca 480
20 gtagtatggg atgcaggttt 500

<210> 371
<211> 529
<212> DNA
25 <213> Enterococcus faecalis

<400> 371
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30 cctgaaaatc aagcagatgc ggcaaaagta acggaaatga tcaatgtcaa aaatcctacc 120
gaaaaacaaa agcaacaaat gagcgattac gttgtaggac ttatcaatga tgttcgcaaa 180
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35 gcaaaaatag ataatcccaa agaatttgat catgacgtaa atgcatcaa tcgtgcagca 300
aaagaaaatg gttttaaaga attcctgga caaaactttt atgaaaacct aagtatggga 360
agatttacga cacaagaagg taaagtttct atgtatgact ttgaaaaagc tgctcgaaat 420
40 gcaattgtaa gcatgttgat gaacgatgga cattctggct attccattt agattcttta 480
ttagatgcaa atgaaacaaa catggcagtt totatttcag gagatttaa 529

45 <210> 372
<211> 558
<212> DNA
<213> Enterococcus faecalis

<400> 372
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agaaaaagac accattgatc aatctgttaa agaccaacaa gcagtggctg atcaaaacaa 180
55 agacgcattg gttcaaagtc aacaagcagt gactgaccaa caagcagttg tagacgaagc 240

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	taaaaaagtc gtggatgaag caacaccttc agccattgaa aaagccaaag agcaagtggc	300
	tactgataca caggtctgttg atgaccaaca aaaagtagta gagcaagctc aaacagacgt	360
5	taaccaacaa caagctggtt ttgatgaaaa agcaaaagaa acgactgctg cttaaagtgc	420
	aaatgataaa gatcaacaag cagtaacagc tgcaaaacaa gaacaagtca agcttgaaga	480
	attagcgaaa aatgcggaag cggaaaaagt aaaggcagaa aaagaacaag cagcaaaaga	540
10	agcagaattg gctaacaa	558
	<210> 373	
	<211> 687	
15	<212> DNA	
	<213> Enterococcus faecalis	
	<400> 373	
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20	tatggattcc caagttgtcc aattgtcaaa cacgttaagt acgcagatga gcaacaaaga	120
	tctcgaacgt agtgacgttg atgcaaattt aaaaaaagcg ttatctgatt tttcaaattgc	180
	agatatttct gaagcgagaa ttgtcgatga taaagggatt attcgggcaa ccaatgattt	240
25	aaatcaacaa aatattattg ggaaaaagaa tgattatcgt gatttaaattg actttacgag	300
	taaaaaatat caagcttttag ataattgataa acgctgtgtat gtgaatgtcc agccgattca	360
	atcgctact ggagaaacag tgattggcgt cctttatgtg aaaagtaatt tagaaaataa	420
30	ataccaagaa attaccaaca cagcaagtat ctttttact gcttctatta ttgccgcagc	480
	aatctcgatt attgtgactt tactgattgc acgatcaatc acgaagccga ttggtgaaat	540
	gcgcgagcaa gccattcgaa tcgctcgttg tgattacgct ggaaaagtag aagtcattgg	600
35	aaaagatgaa ttaggccaat tagcagaaac atttaataca ttatcagaac ggattgaaga	660
	agcacaagaa acaatggaag cagaaag	687
40	<210> 374	
	<211> 534	
	<212> DNA	
	<213> Enterococcus faecalis	
45	<400> 374	
	tatcttagct tcgcaaccag ttactcgttt taggaatgct tttttcaatg aaacggaaga	60
	tatccaaacc aatgaagaca gtcaagactt aacctacacg agtaaagaag aacgattggt	120
	tgcagaagaa aaactgggaa aaattgattt taaagggacc ttgccagaag agaataaacg	180
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55	ttggacaaag acctgggaaa cctggaaaag aacgtgcaag acaagctttg aaaaaagtag	180

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gagaaacgat ggaaagaaac ggactaa 507

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<211> 508
<212> DNA
<213> Enterococcus faecium

<400> 386

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5 tgcagccgct actagcagct tgcagccgat ttattttaca aaagggcatc ctttcgacta 420

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35 <213> Enterococcus faecium

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 <211> 273
 <212> DNA
 <213> *Enterococcus faecium*

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 25 tgtagctatc aatataaata cagaacttac gtattttatt attttacgga acattataac 180
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 <212> DNA
 <213> *Enterococcus faecium*

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<211> 508
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<210> 394
<211> 321
<212> DNA
<213> *Enterococcus faecium*

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aaaatatgaa ttagatcccg g 321

<210> 395
<211> 613
<212> DNA
<213> *Enterococcus faecium*

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	aagagctaga aca	613
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	aacgttagga ttgttaacaa aagatcaaac actagatgag tatcgaaacg agattgttga	360
25	gttattgtta ttagcgcaag aaaggataga tgcaacaaaa	400
30	<210> 397 <211> 533 <212> DNA <213> Enterococcus faecium	
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45	taaagaaagc gtatttataa tgttttcttc agcttctgat aataattgtg agccatcacg	480
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<212> DNA
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atcatcaacg cctgttccca ggccggccac gtcggtaacc cggagctggc ggtgtatagc 180

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	gaacctgatc aacggcctgc ccgccgggca gttgattatc cagcacttcg gcgccacgcc	240
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5

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 <213> *Klebsiella pneumoniae*

40

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 aattcaaatc gttagggttt atctgtcata acgttcgct tgetgcccag tcattcaacg 180
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<210> 435
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 20 ttttaattgc gtatgttgta atggcctata ttcagcaaaa acgaaaagtt ggctgggata 480
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25 <210> 541
 <211> 450
 <212> DNA
 <213> Streptococcus pneumoniae

30 <400> 541
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 tttgaaaatt atgaaggcta accaaacctt gttctctatc acaactagta tcttggaaaa 180
 35 gataaaacca gtttttagaga aggaacaacc agatattgtc ctagttcacg gtgacactac 240
 gacaacttat gcagcagcct tggcagcatt ctatttggga attaaagtag gacatgttga 300
 agctgggttg cgaacgtaca atttaciaaag tccatttctt gaagaattta acaggcaatc 360
 40 gacatcaatc attgcaactt accatTTTgc tccaactgag ttggctaaag aaaatctctt 420
 aaaagaaggt agagagaatg tttatgtgac 450

45 <210> 542
 <211> 565
 <212> DNA
 <213> Streptococcus pneumoniae

50 <400> 542
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 gcagatgaaa gaaaacgttt gggcttgcca cgaaatacca atctaggatt gcatttgatt 180
 55 gatatcatto ctttagatgg agcaccaaat cattcggttt taagaaagat ttacttttTg 240

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	aaagtatact ggtatcgttt tttagcaagc ttaggaacaa cttatgttgg cgaccatgtg	300
5	gatatgcatt ccactaagca aaaactaatt attgggttct ttaaaaaact aggatttgca	360
	aaactatttc ctcaaaattc tgtatacaga cgcttgata atctctatag aaagtatgat	420
	tggaaaaagc agaagtatgc ggggactatc aatgcttctt tatttgctaa agaagttatg	480
10	ccagtagaga tttggggaga aggagtagag aagccttttg aggatacctt ctttaaagtt	540
	ccaacggagt atgatoctga cctga	565
15	<210> 543 <211> 662 <212> DNA <213> Streptococcus pneumoniae	
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	tattttttga ttatttcatt tttgtttatt attgggatta atttacaaaa tcttccatta	180
25	tcaagaaaga tttattttatc attctctatg ttaattattt ctagcttatc caccttaccg	240
	ataaagctaa taaataatct cagtgattta agaaggatat catattactt attgcacagc	300
	atatttttat ctgtattttt aggtttgggt tttaaaatat ctttagtaac agttgctgta	360
30	gagggaattg gcttttcata tggttttaat ggagggttga ctcataaaaa tttttatgca	420
	attacaattt tagtttctta tattctacta tatgtcagca gaaaatatga cgctaaacat	480
	cagattgata gttttgtatt atgggttagat ctttttttac ttttaatatc taatacgcgga	540
35	acagtttata taatactagt tgttttttgg attattatta atagaaattt tataaataat	600
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40	tt	662
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50	aactgggtcca aattcgcaag gagaatagct ggctaattcg agctgacttt gaattgcttg	180
	atacggtgta taaggtcttt gcttatatac gtaaggatgg cgaccgtcgc ttcctagtgtg	240
	tggctaactt gtccaatgaa gagcaagact tgacagtaga aggaaaagtc aaatctgtct	300
55	tgattgaaaa caccctagct caagaagtct ttgaaaaaca aatcttagtt ccatgggatg	360

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<211> 610
<212> DNA
<213> Streptococcus pneumoniae

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acgatttctt ggtcaagaat ccttggtctgc agtaggagcg acgacagcga tttttgacct 180
15 gattgtaggc ttacacttg gtgttgga tggcatgggg attgtcattg ctcgttatta 240
tggggctcgg aatttcacta aaatcaagga agcagtagca gccacctgga ttttaggtgc 300
tcttttgagc attctagtta tgttgctggg ctttcttggc ttgtatcctc tcttgcaata 360
20 cttagatact cctgcagaaa ttcttcctca atcttatcaa tatatttcta tgattgtgac 420
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cagtctagca gccctgggat ttctgatttt ctctgccttg gttaatgtgg ttctggatct 540
25 ctattttatt acgcaattgc atctgggagt tcaatccgca ggacttgcta ccattatttc 600
gcaaggttta 610

30 <210> 546
<211> 546
<212> DNA
<213> Streptococcus pneumoniae

35 <400> 546
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taggccttgg tgtcgctatc atcatcgtaa ccattatcgt gcgcttgatt atcttgccac 180
40 ttggtatcta ccaatcatgg aaggcaacgc ttactctga aaagatgaac gccctcaagc 240
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aagcccaaca agctctcttt gctgctcaaa aagagcacgg tatcagcatg tttggcggtg 360
45 taggatgttt ccctatcctc cttcaaagtc ctttcttctc tgctatctac tttgctgcc 420
aacatactga aggggttgct caagcaagct acctagcat tcctctaggt tctccaagta 480
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50 gagtag 546

55 <210> 547
<211> 262
<212> DNA
<213> Streptococcus pneumoniae

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 5 tttacagctt ggcaacttgaa attggtggca tcacagggtcg agtatggaat aacgacgatg 120
 gcacagtgga aatcttagcc caagcagact catctgctat catggcaaaa tttatccaag 180
 aaatccgaaa aggaccgaca cctttttcaa aagtaagcta cttagatgtc aaactaagca 240
 10 actttcctcc ctactctgac tt 262

 <210> 548
 <211> 629
 <212> DNA
 <213> Streptococcus pneumoniae
 15

 <400> 548
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 20 tctccatccg aagacttggc ttcaatctgt gaagctgagg gaactaaatc ctcgtttgaa 120
 gcgtagtaaa gggttacacg gtaacggaca cgcttgtttt ggtccaaggc tttacgcacc 180
 ttgctttcat agtagttttg accagtcgaa tactcggcct gtgcctgatt tgcccaggct 240
 25 gtctgaacag caatgttttt aggattgctt gttgaggcat caaaaccatc caaaccaccg 300
 attaaggcat agcctaacaa atgacctcta tcgactgcat ggggtataaga gccctttaga 360
 ttcttgacct gatgccaaac tggaggagtc caagaagttg aaccattccc agtttcttta 420
 30 cgattcttgt actgacgagt ggccttagac aagagggcat tagctacggt tggaacagtt 480
 tccttgccca ctgtctttgt tttattgtca gcgtagggct tacttgaaac cttggcatct 540
 agatttgttt tattaccatt gacgataaaa gcacctgagc cattccactc cagactcccc 600
 35 tttatttgac tcttgactgc gtctgttaa 629

 <210> 549
 <211> 323
 <212> DNA
 <213> Streptococcus pneumoniae
 40

 <400> 549
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 45 gcctgcccg aaaggctatg ctggaaccat gttcctttat aagaaagaac ttacacctac 120
 tatcagcttc ccagaaatcg gtgccccttc taccatggac ttggaaggtc gtatcatcac 180
 tctagaattt gatgcatttt tcgtaacca agtttacact ccaaacgctg gtgacggctc 240
 50 caaacgcttg gaagaacgcc aagtctggga tgccaaatat gctgagtatt tggctgaact 300
 agacaaagaa aaaccagtcc ttg 323

 <210> 550
 <211> 206
 55

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<212> DNA
<213> Streptococcus pneumoniae

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gtcattcaag aaatgttgat tcatgatgca cctaagtatg gtaatgatga tgattatgct 180
10 gacaaattgg ttactgctgc ttatga 206

<210> 551
<211> 510
<212> DNA
15 <213> Streptococcus pneumoniae

<400> 551
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ccctatggat tgatcaaata aagcaaggga atcctataac gattacggaa cctagtatga 180
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25 gaaaaacagg agatatccta gtacagaaag caccagcatg taccattgaa gtgttggcgc 300
aagctgttac ggaacttttt gcacctaatac aagatattaa agtaatcggg attcgccacg 360
gtgaaaagat gtatgaaacg ttgttgacta ctgaagaatg tacgaatgcc attgatttag 420
30 gcggctttta tcgtgtgcct agcgataatac gagatcttaa ctatgataag tatttcaacg 480
aaggggatgc caaacgcaat cccttaatat 510

<210> 552
<211> 589
<212> DNA
35 <213> Streptococcus pneumoniae

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atttagctgg tgtcaatcgt ccacagaatac ctgatgaatt catggaggga aattacggtt 180
45 tttcaagtag attattggag atttttagaaa agtatgaaaa cacttgtcct gttctactct 240
caagttctac tcaagctagt ttagaaggcc gattttcaaa ctctatatat ggacaatcta 300
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50 tttaccgttt cccgaatctt tatgggaagt ggtgccgtcc taactacaat tctgctgtag 420
caactttctg tcataatcta gctcacgatt tacctattca agtaaatgat ccaagtgtag 480
aattggagtt gctgtatatt gatgatttga tacaagagtg tctaactgca ttggaaggaa 540
55 atcctcatcg ttgtaatcta gatggattac aaatcttacc tagcccatc 589

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5 <210> 553
 <211> 545
 <212> DNA
 <213> Streptococcus pneumoniae

 <400> 553
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 taaaaattga tgaatcaaatt taaaccagat gctttattga ttttagggga taaaaattct 120
 tgtttatcag ctattactgc caagcgttta catattccaa tttttcatat ggaggctggc 180
 aatcgctgta aggatgagtg cctgccggaa gagactaatc gtoggattgt tgatattatt 240
 15 tcagatgtta acttagcata ctctgaacat gcacgtaagt atttacatga gtgtgggtta 300
 cctaaagagc gcacatatgt aacaggttct cctatggcag aagtgttaca taaaaattta 360
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 20 ttactttcag ctcaccgtga ggaaaatatt gatacagata aaaattttat ttctctcttt 480
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 25 agatc 545

 <210> 554
 <211> 250
 <212> DNA
 30 <213> Streptococcus pneumoniae

 <400> 554
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 35 ataaagtatg ttactttaac tacgaacaca gaaaaaattt agtagaagct attcgatatg 180
 tcgatttagt aatccctgaa actagttggg aacagaaaaa gtcagatggt aaagactacc 240
 40 atattgacac 250

 <210> 555
 <211> 283
 <212> DNA
 45 <213> Streptococcus pneumoniae

 <400> 555
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 50 ctacgtgaac atcctatttg gatggcagaa gaagagattg aatcaggcat ctatgagatg 180
 tgcgacatgc tccttttgac caaggaagtt tctatcaaga aataccgagc agagctggct 240
 55 atcatgatgt ctgcaagcg atctatcaag gccaatcatc gta 283

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<210> 556
 <211> 284
 <212> DNA
 <213> Streptococcus pneumoniae

5

<400> 556
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 gaggttcgtt cattattaaa tgaggcacga aataaagctg ctgaaattat tcagtcaaatt 120
 10 cgtgaaactc acaagttaat tgcagaagca ttattgaaat acgaaacatt ggatagtaca 180
 caaattaaag ctctttacga aacaggaaaag atgcctgaag cagtagaaga ggaatctcat 240
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15

<210> 557
 <211> 627
 <212> DNA
 <213> Streptococcus pneumoniae

20

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 25 ctcataagct aggaactaag aaaactgacc tcccatctag tgatcgagaa ttttacaata 180
 aggcttatga ctactagca agaattcacc aagatttact tgataataaa ggtcgacaag 240
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 30 tcaagttagt ggaagatatt cttgccttct tagctccgat tcgtcatcca gaacgttttag 360
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 gcaagtacac agcagaagac gggtatatct ttgatcctcg tgatataacc agtgatgagg 480
 35 gggatgecta tgtaactcca catatgaccc atagccactg gattaaaaaa gatagtttgt 540
 ctgaagctga gagagcggca gccaggcgtt atgctaaaga gaaagggttg acccctcctt 600
 cgacagacca tcaggattca ggaaata 627

40

<210> 558
 <211> 784
 <212> DNA
 <213> Streptococcus pneumoniae

45

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 50 ctctctgtga ccaagaattt tatgataaag catataatct gttaactgag gctcataaag 180
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 55 caccaattac ccatccagag cgacttggca aaccaaattc tcaaattgag tatactgaag 360

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	ctaaagaaaa aggtatccta cctccatctc cagacgcaga tgttaaagca aatccaactg	600
10	gagatagtgc agcagctatt tacaatcgtg tgaaagggga aaaacgaatt ccaactcgttc	660
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	tcttcagcat ctgatggtta tatTTTTaat ccaaagata tcggtgaaga aacggctaca	240
30	gcttatattg taagacatgg tgatcatttc cattacattc caaatcaaa tcaaattggg	300
	caaccgactc ttcaaacaa tagtctagca acaccttctc catctcttcc aatcaatcca	360
	ggaacttcac atgagaaaca tgaagaagat ggatacggat ttgatgctaa tcgtattatc	420
35	gctgaagatg aatcaggttt tgtcatgagt cacggagacc acaatcatta tttcttcaag	480
	aaggacttga cagaagagca aa	502
	<210> 560	
40	<211> 462	
	<212> DNA	
	<213> Streptococcus pneumoniae	
	<400> 560	
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	aataaatagt ctctatatca gaagacagct gatgattgta gtaatcaaaa ctggcttcat	180
50	attgcaaadc cgacgcattc ctcaaaccac gcactagaca agtagcacc aatctTTTTg	240
	caacatcgac caccaattca tcatgagaag ccacgacttc aacattttcc agatgtccca	300
	aagccttttc tagccccgt ttacgatttt cgataggaag aaatccttgt ttgtggggat	360
55	taaaaaaat acccacataa agcttatcaa aaagtctgct cgcccgttca atgatatcca	420

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5 <210> 561
<211> 508
<212> DNA
<213> Streptococcus pneumoniae

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20 tggacgataa ttaacaccaa taccgccaga aagattgata aagtctagcc aaatgccccaa 420
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25 <210> 562
<211> 652
<212> DNA
<213> Streptococcus pneumoniae

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35 tctagaaaag ccattggtg caaaattagg gactttgggt cttcctacta gtcaaaaaaa 180
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45 aataaatggg agttgggtact attatagaca acatgataaa caaacgggtt ggcaggagat 540
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50 <210> 563
<211> 250
<212> DNA
<213> Streptococcus pneumoniae

55 <400> 563

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 5 caaggtacag tggattcctt gttccttagc cttggtgaag agagcaatca ggaaatcaat 180
 ctgcaagaga gcttctctc cactgactgt aatcccaccc ttatttcccc agaaaccacg 240
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 10
 <210> 564
 <211> 500
 <212> DNA
 <213> Streptococcus pneumoniae
 15
 <400> 564
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 20 catcaaccta ccttgatatc atcaaaccat ctgtaggaga aagtactaaa acatatttag 180
 ggtttgactc aggggaagat aatgtagctg ctaaaaaagt aggtctatat gactacgaaa 240
 aattggttac tgaggctggt gatgaggcta cagatgttgc taaacgctat gataaatacg 300
 25 ctgcagccca agcttggttg acagatagtg ctttgattat tocaactaca tctcgtacag 360
 ggcgtccaat cttgtctaag atggtaccat ttacaatacc atttgcattg tcaggaaata 420
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 30 tagatgaata ccaaaaagct 500
 <210> 565
 <211> 525
 35 <212> DNA
 <213> Streptococcus pneumoniae
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 cccaaggaga tcatacggac tcatttgtga ataaaaacac agaaaatccc aaaaaagaag 240
 45 ataaagttgt ctatattgct gaatttaaag ataaagaatc tggagaaaaa gcaatcaagg 300
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<212> DNA
<213> Streptococcus pneumoniae

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ttgaacttga aattgctgag ttcgatgtga aagttaaaga agcggagctt gaactagtaa 180
10 aagaggaagc taaagaatct cgaaacgagg gcacaattaa gcaagcaaaa gagaaagttg 240
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<213> Streptococcus pneumoniae

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agaagctaaa cgaaaagcag aagcagaaga agttaagat aaactaaaga ggcggaacaaa 180
25 acgagcagtt cctggagagc cagcaacacc tgataaaaaa gaaaatgatg cgaagtcttc 240
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<211> 414
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gctacacctg ccagttctga gtcgaactcg cgcaagagac taatcatacc gttgaccgtt 180
40 ccgccacctt tcaagaagtc atccacaatc aagacacggc tgcttgcctt aagactacgt 240
tttgaaagga acatthttctc gatacgggtca ccacttgaac ctgaaacata gttgacgcta 300
acagttgaac cttcggtaat tttcaggtca cggcgacaaa tgacaaaaga gacattgagg 360
45 acattggcaa ctgcatttgc aagtggcaca cccttagttg ctacggtcac aacc 414

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<211> 312
<212> DNA
<213> Streptococcus pneumoniae

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	ccacttggtt ccatcaactc tatgggcttg ccaaataatg gcttagacta ttatttggat	180
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5	atgtctccag aggaaaccca tactattttg aaaaaagtcc aagagagtga ttttcgtggt	300
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	gcaagctggg cgaaaaacta ggtgctttta aattgccagt agaagtgggt cagtatgggtg	360
25	cagagcaggt ctttcgtcat tttgaacgag ctggctacaa accaagtttc cgtgaaaaag	420
	acggccaacg ttttgtgacc gatatgcaga attttatcat tgacctcgcc ttggatgtca	480
	ttgaaaatcc aattgctttt ggacaagaat tggaccatgt cgttgggtgt gtggagcatg	540
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 15 cagggttactc aaagtctgac agctttcgga ggagatgcta gaagagctgt ggatggcaaa 480
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 <213> Streptococcus pneumoniae

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 40 aaaaacagcc tctatggact g 561

 45 <210> 574
 <211> 503
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 agatggaaaa gtcaaagaag tcagtgatat agagacgatc gttttgtgga ttttgaaaga 240
 55 cattgattcc ctcaacaatt acaaaatcag cagctttgac actttgtttc tcttcgggta 300

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	tgcaacatta gatggtaatg aagcttatcg agatgctgac tttgtcataa ttgctgtccc	240
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55	accagtctgc tagctgaaat taaccgtaag ccagaagacc tggatgccat cttgattacc	180
	catgagcatt cagatcatat ccatggagta ggcgttttgg ctgcgaagta tgggtatggat	240

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	tagcagaggg	ggagatagta	aactttgcga	ctcatgaggt	ggtcgatgaa	gtctttatca	480
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	actttcctac attggtttta ttcgttttca agaacaaaat aaaaaataa tcgatttttt	480
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	cagggtgttg gtataccaat tgacaagcca atgtttaatg ctggagttat gcttattaat	420
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	gtctcatgat aattattttg caaagtttgc actagagtat gggaagggtg tgttct	596
55		

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 <211> 530
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 <213> Streptococcus pneumoniae

5

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 <211> 380
 <212> DNA
 <213> Streptococcus pneumoniae

25

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45

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<210> 588
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5

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 <212> DNA
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25

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<210> 590
 <211> 516
 <212> DNA
 <213> Streptococcus pneumoniae

50

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 55 ctaaatcttg ttatgttatt tctttatata cgtgaaattc agaaagtagt attgttttca 180

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 <213> Streptococcus agalactiae

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 35 ttaacaaaga acaaaaatca ctgattttca aaatatttaa aacaaaacca ttaactataa 240
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 40 aatatagaac gttagggtagc aatgtttatt taaaagttca tcctagagat gtagtagatt 420
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 55 tatgcttttt attggccttc agacgagcgg ttctttaagt tcagcccggg tcaaatacgg 180

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<213> Streptococcus agalactiae

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	aggagtatat ctctcaattg gctcggtagg aaaagcatta caacagggtta tgacatgggt	180
10	tccattgact caaatcaatt ctcttttgaa acaggtctta atgaagggtt ctattgcgaa	240
	ggtatttgac aaagccaacg aagccactgt ctctaactat aaagaatcat atggtgttgt	300
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<211> 535

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	aactgaagtt ttctaataac tataccgaaa tcagtaacta caataaacc tccttagctt	180
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30	gatcattgag tagtcacctc cctaagatat tgaatacgtt tcgtatttcg aattattatg	300
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35	gtgcttcact tccttattat ttaaaaatga gcttggttca aatggaaatt gctaagttag	480
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	tgactttcta caaatttgat gataaatatt ggttggctag tcataaagct ttggattctt	180
50	atttagacaa catcaatttt gactataaccg taacagatat ttctgacgag tataaaatgc	240
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	caacacttaa ttttcgtact ttgatagaga tgacttataa aggtgagaaa ggttatcttg	360
55	ctagatttgg tttttctgga gaatttggct atcaattttt cctaccatct totatttttg	420

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ctacttttgt ttcggatgtc tgtgaaggta tagcagagtg tggggatgaa cttgatagat 480

atthaagggt tgaagtggga caaccatta ctgatattt 519

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tgcttcttca ggtgttaatt taaaagctta tcataatatt gctgtgtgtt tagggacctc 240

acttggggga aagagtgtcg gtcaaaatgc cttgtatcaa tttgaagaag gagagcgtca 300

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agtagatgct agtttattag aaaaagcatc tgtttaccat attgctgatg aattgatggc 360

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25

tgccgtaata ttaggaacac aattacttca agatggcgat tgtgatttag ctatttgtgg 480

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ctgtcaacco agcacaattt aggaaaatgg atgatttttc caaaatggtt gccgtaacaa 180

cagctcaagc actaatagaa agcaatatta atctaaaaaa acaagatact tcaaaagtag 240

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caaatagtgg agcgcttgat ggtatacaat atgccaagga aatgatgcgt aacgataatc 480

50

tagactatgt gattcttgtt tctgctaata agtggacaga catgagtttt atgtgggtggc 540

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<210> 623

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20 ataattgtagg tttttcaaaa tgcagccaaa ttaatcaaga caataagact gtactgctca 540
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cctgtactaa aataatttta tcatgagttg gatttggaat aatagcatag acaccaaadc 180
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attaaaggct ctgaaattat ttaaattctcc aaagaaatca tcaaagaaag gattgatgcc 180
accaggcgca tgtgaaacat gatttaaacc tgaaaaaagt ggattattag ggtcagtttt 240

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	aacatccatg ggatacagaa gtagaagagt tggttatcct tggagaccat gttacaacag	600
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 caaagataat gttcagggaa cagattatga aaaacgggtt aatgaggcta ttactagcgt 240
 ggaaaaatta aagacttcat tgcgtgccaa ccttgagaca gtttatgatt tgaattctat 300
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 cacaaaaagt gaacattgat ccactaaaa aatatgaggt caagtttgat attgaaacaa 180
 55 gtaacaaggc tggacaagct ttccttcgta ttatggagaa aaaagataac aatacgcgac 240

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	acccaaagtt agatgtctcc gaggtgacac ttgaacttta ttatgaaaaa ggaacaggtt	360
5	ctgttacttt tgataatata tcaatgaaag caaaaggccc taaagactca gagcatccac	420
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	cgacagatcc tcaaatacgaa aaagatttag agaaagctga tttattgacg ctaactgttg	240
	gtggtaatga tgtcttggct gttattcgta aagagctcag tcatttatca ctaaattcct	300
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	aagataatcc taaattgcct atttatgttt taggcattta taatcctttt tacctaaact	420
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30	tagttgatgc ttcagaaaat gtttattttg tcccaattaa tgaccgcctt tataagggaa	540
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	gcgacacct cactaaaaaa ccgcatcaca ttgagattga taaaaaatta gatgttgatc	480
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 55 aaagttatat tccctaattt tatgccagct acctcgcttc tacgcaatcc aagatatgtt 420

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5 ttaaattctt gcattgatct acgtttg 507

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<213> Streptococcus pyogenes

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10 gttttgacct attcattagg tgcaggattt tggaatttga ttctagcttt ctgtatcact 240

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15 ctgcctcaat tggtttcagt tatcatgact atgttgtcac aaatgctacc agtttatgta 420

tcttctgaga cttcttattc cttctttggg attggtttac caaccaccac tccaagttta 480

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ttgaaaaagc acctccggcg attaacgtat ctgagactca ttgggccaaa acatggcttt 240

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<212> DNA

40 <213> Streptococcus pyogenes

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 <213> Streptococcus pyogenes

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	tccagcaatg gctacagctg ctgatgataa aataagaacc aaaatcataa agactgcact	180
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	ctagcccaat agcagtatta tcagctaata ccataatatt aaggaaatgg gcttgactat	300
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	gaccaacaag agcaaccatt agacttgaaa gcatggtagt aacagctaca ccagtaagaa	480
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10 tcaagcaaag cagataaaag cgctgtttac tcaaaagcag agtcaaaaat agagctagac 240

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15 gaaggtgctg ctatggtgat gtatacaaat aaagatacta ctgatggacc attgatgatt 420

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actaatgctg taaatattgt aatgcgccag ccaagcgcac ctaatttttc ctcggcactt 540

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gccgccactg ttgcttattc ctcgtaacg ggtggagcgg tcaatattga cttgtcgtct 240

35 accagaggtg ctggtgttgt tgtotattct gacaatgata ccagtgatgg gccgttaatg 300

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acaacaaatg cggttaatat tgcgatgcgt cacgcaacca cccccaattt ttcacggcg 420

40 cttaatatta ctacggcaa tgaaaatggt agtgcaatgc agctacgagg gtcagaaaaa 480

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<211> 516

<212> DNA

45 <213> Streptococcus pyogenes

<400> 666

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	ttaagccaga tattgcagca cccggccaag atattttgtc atcagtggtt aacaacaagt	480
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 35 tgattggaac tacttgtcag aaggaaaagt cacagcatat acgtacggcg gaataacacc 180
 ctacaaaaaa actthcaatac thaaaaatat cctgtthaat thattggatta atggaaagca 240
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 40 tgatctaaag gthtagaaaat ththaatagc acaacatcaa thtatththt ctggthtctag 360
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 45 ththththtata acaggatata gagataaaga aagthththt aaagthataca aagacaataa 480
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55	tcatgaaggg aatcatttag aaattcctaa aaagatagtc gttaaagtat caatcgatgg	360

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<213> Streptococcus viridans

25 <400> 689
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40 <213> Streptococcus viridans

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<210> 691
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 agttattgct gttgatgatt tcccaattga caatcttcaa gtcccagtaa ttcagtatag 360
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 <212> DNA
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<211> 400
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35 caatctgtgc taattttgac a 381

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55 tattaaagag attaactctg accaacataa aattgtcact ggcatagca ataaaactat 480

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20 taagcaggaa ctaaaagatc tctacatgga taaggctgat tttaaag 407

25 <210> 701
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<212> DNA
<213> Streptococcus viridans

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40 <210> 702
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<211> 615
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55 <400> 703
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 45 <210> 710
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 55 aagtacttcc tcgattgggc aaagtcactg ctccgatatt gatatttggg tctgtcacca 360

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 aaaaatatta acagcaatga ttgggttaaa taacaaaaca ttagacgata aaacaagtta 360
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 20 atatgaagtg gtaaattggt atatcgactt aaaacaagca atagaatcat cagataacat 480
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 40 acgacctacc ttaaatgcag atactaaaga aggaatcact gaggactttg tttggcgtga 360
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	acgcaatgat cgtgttgga aatcttacct agaatatcaa tatgaagatg tattgcgtgg	300
	taagaagaaa gaaatgaaat acacaacgga caaatctggt aaagttacat cttcagaagt	360
10	gttaaatcct ggcgctcgcg gtcaagattt gaaattaacg atcgatatag atcttcaaaa	420
	agaagtagaa gcattattag ataaacaaat taagaagctt cgcagtcaag gtgccaaaga	480
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	tcaatttgcg gttggatctt ctgtaaaagg tggaacatta ttagccggtt atcagaataa	660
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	agtcaaagct agtgatgttc aagtcaaaaa ggcgaaagac aatcaatata catttaccta	240
	taaattatcg atgagcactc ctttaggcga aatgaaagat ttgtcttatc aatcaagtat	300
35	cgccaagaaa ggcgatacct accaaatcgc ttggaagccg tctttaattt ttccagatat	360
	gtcaggaaat gataaaattt cgattcaagt agataatgcc aaacgtggag aaattgtcga	420
	tcgtaatggg agtgggctag caattaacaa agtgtttgac gaagtggcg tagtgcttgg	480
40	caaactcggg tctggcgcag aaaaaacagc caatatcaaa gcttttagtg ataagttcgg	540
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	<211> 660	
	<212> DNA	
	<213> Enterococcus faecium	
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55	aaaagctgga tcaactggtg cgacaacgcc aaaaaccggg gatcttcttg cgcttgctag	180

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	agtaacgcgt gtcagtgatg tatcacaagt agacttaaaa actgctttga tctattccga	480
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	<213> Enterococcus faecalis	
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	gcagatttga aaaagaaaaa aatttcaggt gtttatttca atgaacatcc agccagatta	420
	tatcccaatg gtcagtttgc ttctcacttt attggctata caaaagcagc caatccagat	480
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	aaaaaccatt cgtacactta taacgagatt gtataaaaag ggatttatag atcgtaaaaa	180
	agacaataaa attttttaat attactctct tgtagaagaa agtgatataa aatataaaac	240
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<212> DNA
<213> Streptococcus pneumoniae

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	atggtaaaga cctcaataat ttaagtttac ctcagttagc cttgctggct ggaatgcctc	180
10	aggcaccaaa ccaatatgac ccctattcac atccagaagc agcccaagac cgccgaaact	240
	tggctcttctc tgaatgaaa aatcaaggct acatctctgc tgaacagtat gagaagcag	300
	tcaatacacc aattactgat ggactacaaa gtctcaaatac agcaagtaat taccctgctt	360
15	acatggataa ttacctcaag gaagtcata atcaagttga agaagaaaca ggatataacc	420
	tgctcacaac tgggatggat gtctacacaa atgtagacca agaagctcaa aaacatctgt	480
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<213> Staphylococcus aureus

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30	cgattagaac attaatcaca agactatata aaaaagagat tataaaacga tacaatcag	180
	agaatattta tttttactca tcaaatatta aagaagacga tattaaaatg aaaactgcta	240
	aaacctttct taataaactg tatggagggg acatgaaaag tttagtgtctg aattttgcga	300
35	aaaatgaaga attaaataac aaagaaattg aagaattgcg agacatttta aatga	355

<210> 815
<211> 702
<212> DNA
<213> Escherichia coli

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	ccgggcaaga gcaactcggc cgccgcatac actattctca gaatgacttg gttaagtact	180
	caccagtcac agaaaagcat cttacggatg gcatgacagt aagagaatta tgcagtgtctg	240
50	ccataaccat gagtataaac actgctgcca acttacttct gacaacgacg ggaggaccga	300
	aggagctaac cgcttttttg cacaacatgg gggatcatgt aactcgcctt gatcgttggg	360
	aaccggagct gaatgaagcc ataccaaagc acgagcgtga caccacgacg cctgcagcaa	420
55	tggcaacaac gttgcgcaaa ctattaactg gcgaactact tactctagct tcccggcaac	480

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	aattaataga ctggatggag gcggataaag ttgcaggacc acttctgcgc tcggcccttc	540
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	ttgcagcact ggggccagat ggtaagccct cccgtatcgt agttatctac acgacgggga	660
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25	cgctgaatac cgccatcccg ggcgatgagc gtgataccag cagccgctg gcgatggctg	360
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	tacactatct acttcaccct aaaatagcag gatacgggtt agccttatcg attttctttt	180
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	ctctgttttg cattcaattc cagccttctg aactggcaaa tctttttttg attttttatt	300
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	tcctttcgat tgcgtgggtc atattttggg cagcggcggt tccattttaa aaagggatct	480
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55	gaaataaagg ttggcttc	558

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 5 <213> *Staphylococcus aureus*

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 ttgttgatta tagtaataaa gaagcgttaa atgcattggt agacagtgca aaagaaattg 240
 15 ctaaagctga gaaagcgtat gcaattaaaa tcgatcctga tgttgaagtt gataaaggta 300
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 20 atgagttatt aaatagtttt gaacgccgaa atcggtcaca agtgcgcttg gctttaaagc 480
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 25 atgatgcgtt gcatgaagat ggagatgctg aactatTTTT agtaaagttg gacccaaaag 660
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 agcagaagat ggaacatct gaaaagcaag 750
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 <210> 819
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 35 <213> *Proteus vulgaris*

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 40 agccaagggtc gtttaggtgt tgctttaatc aacacggaag ataattcaca aataacatat 180
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 50 <210> 820
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 <212> DNA
 <213> *Staphylococcus haemolyticus*

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	tttaaatacac atggatatga acaccatgga tttactactg aatatgacac atcaagtcaa	360
10	gcaagatgga tgggtggttag ctatctaaaa ggggaaacac ctgcttcatt aagaaaacaa	420
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	tcctttatac ccatagactg gatatagtca tgcaaagcag ctgggtccacc aaccagttca	360
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40	tgatgcagta ccaacatagc taaatgcaat ttaaatacac tttgcattgg gaatttttca	600
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	<211> 340	
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	agtcggccat ggcgaactat gcctacggct attcgaagga agataagccc atccgggtca	240
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	ttttcaattt ctcttgaaaa catTTTTtGct ggtgctaattg caactcctcc ttcataaata	180
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	atatttgctt tttcaaacca ttgcaaccac tcatcttctc gataagagcg atacaagttt	300
	tcatttatta gatcagtttg atgttgtaaa cgtttcgccg taccgatga acacaatacc	360
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	gcatcatccg tcattttctaa acctogaggt aagcgcttaa aaagaataac gccaagccgc	720
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	cctgatggag taaagattga tgcagaaaaa tcttttagatt tagatggcgt atatataaaa	480
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55	gaagaagggg actttgggag gattagaa	568

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 5 <213> *Staphylococcus aureus*

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 tcaaatatTT ttatacacat cgcgggccag tgatggatta tacaatcaa tcattagtag 240
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 20 taggttatga ttcaatgagc caaatccggt ggctgtcagt gttagattta aaagataaga 480
 ctgaagacca acttttaaaa gaaatggatt atcaaacgag acgtaatat taaaaaacat 540
 atgatattgg tgtaaaaact aaaacgttaa cgattgatga aacgcaaact tttttcgact 600
 25 tattccatat ggctgaggaa aagcacgggt tcaaattccg tgagttacca tactttgaag 660
 aaatgcaaaa gttatacgat gaccacgcca tgtaaagtt ggcgatatatt gatttaaacg 720
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 30
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 <212> DNA
 35 <213> *Staphylococcus epidermidis*
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 40 aattccatta ataccatttt acaaaatatc gaattttaca ttttcaaaag atatgatgaa 180
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 <211> 810

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<212> DNA
<213> Staphylococcus aureus

<400> 827

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	agtaaaattt aattcagata agagatttgc ctatgcttca acttcaaaag cgataaatag	180
10	tgctattttg ttagaacaag taccttataa taagttaaata aaaaaagtac atattaacaa	240
	agatgatata gttgcttatt ctctattttt agaaaaatat gtaggaaaag atatcacttt	300
	aaaagcactt attgaggctt caatgacata tagtgataat acagcaaaca ataaaattat	360
15	aaaagaaatc ggtggaatca aaaaagttaa acaacgtcta aaagaactag gagataaagt	420
	aacaaatcca gttagatatg agatagaatt aaattactat tcaccaaaga gcaaaaaaga	480
	tacttcaaca cctgctgctt tcggtgaagac tttaaataaaa cttatcgcaa atggaaaatt	540
20	aagcaaagaa aacaaaaaat tcttacttga tttaatgtta aataataaaa gcggagatac	600
	tttaattaaa gacggtgttc caaaagacta taagggttgct gataaaagtg gtcaagcaat	660
	aacatatgct tctagaaatg atgttgcttt tgtttatcct aagggccaat ctgaacctat	720
25	tgttttagtc atttttacga ataaagacaa taaaagtgat aagccaatg ataagttgat	780
	aagtgaacc gccaaagagt taatgaagga	810

<210> 828
<211> 565
<212> DNA
<213> Plasmid RGN238

<400> 828

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	ttatcactta tggcatttga tgcggaaata atagatcaga aaaccatatt caaatgggat	180
40	aaaaccccca aaggaatgga gatctggaac agcaatcata caccaaagac gtggatgcaa	240
	ttttctgttg tttgggtttc gcaagaaata acccaaaaaa ttagattaaa taaaatcaag	300
	aattatctca aagattttga ttatggaaat caagacttct ctggagataa agaaagaaac	360
45	aacggattaa cagaagcatg gctcgaaagt agcttaaaaa tttcaccaga agaacaatt	420
	caattcctgc gtaaaattat taatcacaat ctcccagtta aaaactcagc catagaaaac	480
50	accatagaga acatgtatct acaagatctg gataatagta caaaactgta tgggaaaact	540
	ggtgcaggat tcacagcaaa tagaa	565

<210> 829
<211> 226
<212> DNA

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<213> *Klebsiella pneumoniae*

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ggtgggagac atgacccagg gactgggctg ggagagttac gcctatccgg tgaccgagca 180
10 gacattgctg gcgggtaacg caccggcggt gagcttccag gccaat 226

<210> 830
<211> 502
<212> DNA
15 <213> *Proteus mirabilis*

<400> 830
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20 gccgcataca ctattctcag aatgacttgg ttaagtactc accagtcaca gaaaagcatc 180
ttacggatgg catgacagta agagaattat gcagtgtgct cataaccatg agtgataaca 240
25 ctgcgggcaa cttacttctg acaacgatcg gaggaccgaa ggagctaacc gcttttttgc 300
acaacatggg ggatcatgta acccgccttg atcgttggga accggagctg aatgaagcca 360
taccaaacga cgagcgtgac accacgacgc ctgcagcaat ggcaacaacg ttgcgcaaac 420
30 tattaactgg cgaactactt actctagctt cccggcaaca attaatagac tggatggagg 480
cggataaagt tgcaggacca ct 502

<210> 831
35 <211> 391
<212> DNA
<213> *Staphylococcus warneri*

<400> 831
40 agttgaaaat gaaatatgta taagaacttt aatagatgat gattttcctt tgatgttaaa 60
atggttaact gatgaaagag tattagaatt ttatggtggt agagataaaa aatatacatt 120
agaatcatta aaaaaacatt atacagagcc ttgggaagat gaagttttta gagtaattat 180
45 tgaatataac aatgttccta ttggatatgg acaaatatat aaaatgtatg atgagttata 240
tactgattat cattatccaa aaactgatga gatagtctat ggtatggatc aatttatagg 300
agagccaaat tattggagta aaggaattgg tacaagatat attaaattga tttttgaatt 360
50 tttgaaaaaa gaaagaaatg ctaatgcagt t 391

<210> 832
<211> 380
55 <212> DNA
<213> *Pseudomonas aeruginosa*

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	<400> 832	
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	acctcgggaa cttgctccgt agtaggacat tcacgcgcgt tgctgccttc gagcaagaag	180
	cggttgttg cgtctctcgc gcttacgttc tgcccaagtt tgagcaggcg cgtagtgaga	240
10	tctatatcta tgatctcgca gtctccggcg agcaccgccg gcagggcatt gccaccgcgc	300
	tcatcaatct cctcaagcat gaggccaacg cgcttggtgc ttacgtgatc tacgtgcaag	360
	cggattacgg tgacgatccc	380
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	<211> 616	
	<212> DNA	
	<213> Escherichia coli	
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	acctggccgc cgttcgatcc cgcaacggcc gggacttacc gtgggttcgg cctgctgaat	120
25	cagtttctgg ttcaagcccc cggcgcgcgg cgcagcgcgc aaccgatgc atcgatggtc	180
	gcggttggtc cactggctga aacgctgacg gagcctcaca agctcgggtca cgccttgggg	240
	gaagggtcgc ccgtcgagcg gtctgttcgc cttggcggga aggcctgct gttgggtgcg	300
30	ccgctaaact ccgttaccgc attgcactac gccgaggcgg ttgccgatat ccccaacaaa	360
	cggcgggtga cgtatgagat gccgatgctt ggaagcaacg gcgaagtgc ctggaaaacg	420
	gcatcggatt acgattcaaa cggcattctc gattgctttg ctatcgaagg aaagccggat	480
35	gcggtcgaaa ctatagcaaa tgcttacgtg aagctcggtc gccatcgaga aggtgtcgtg	540
	ggctttgctc agtgctacct gttcgacgog caggacatcg tgacgttcgg cgtcacctat	600
	cttgagaagc atttcg	616
40	<210> 834	
	<211> 707	
	<212> DNA	
	<213> Escherichia coli	
45	<400> 834	
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50	ggttgctcgg tcgtgagaac aatctgatgt tgctcgaata tgccggggag cgaatgctct	180
	ctcacatcgt tgccgagcac ggcgactacc aggcgaccga aattgcagcg gaactaatgg	240
	cgaactgtat gcccgcatct gaggaccct gccttctgcc cttctcccga tccgggatcg	300
55	ctttgcagct ttgtttcagc gggcgcgcga atgatcaaaa cgcaggttgt caaactgact	360

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	acgtccacgc ggcgattata gccgatcaaa tgatgagcaa tgccctcgaa ctgcgtgggc	420
	tacatggcga tctgcatcat gaaaacatca tgttctccag tcgcggctgg ctggtgaaag	480
5	atcccgtcgg tctggtcggt gaagtgggct ttggcgccgc aaatatgttc tacgatccgg	540
	ctgacagaga cgacctttgt ctcgatccta gacgcattgc acagatggcg gacgcattct	600
	ctcgtgcgct ggacgtcgat ccgcgtcgcc tgctcgaaca ggcgtagct tatgggtgcc	660
10	tttccgcagc ttggaacgcg gatggagaag aggagcaacg cagtcta	707
	<210> 835	
	<211> 545	
15	<212> DNA	
	<213> Enterococcus faecalis	
	<400> 835	
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20	acgttgctgg ccgtacattt gtacggctcc gcagtggatg gcggcctgaa gccacacagt	120
	gatattgatt tgctggttac ggtgaccgta aggcttgatg aaacaacgcg gcgagctttg	180
	atcaacgacc ttttgaaaac ttcggcttcc cctggagaga gcgagattct ccgcgctgta	240
25	gaagtcacca ttgttggtgca cgacgacatc attccgtggc gttatccagc taagcgcgaa	300
	ctgcaatttg gagaatggca gcgcaatgac attcttgag gtatcttcga gccagccacg	360
	atcgacattg atctggctat cttgctgaca aaagcaagag aacatagcgt tgccttggtgta	420
30	gggccagcgg cggaggaact ctttgatccg gttcctgaac aggatctatt tgaggcgcta	480
	aatgaaacct taacgctatg gaactcgccg cccgactggg ctggcgatga gcgaaatgta	540
35	gtgct	545
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	<211> 515	
	<212> DNA	
40	<213> Escherichia coli	
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	gcaggtcaca ttgatacaca aaattctagc tgccgcagat gagcgaaatc tgccgctctg	60
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45	tattgatctg acgtttcccg gcgagaggcg cggcgagctc gaggcaatag ttgaaatgct	180
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	acttgactgc gaacctgctt ggtgggcaga cgaagcgtat gaaatcgcg aggctccgca	300
50	gggctcgtgc ccagaggcgg ctgagggcgt catcgccggg cggccagtcg gttgtaacag	360
	ctgggaggcg atcatctggg attactttta ctatgccgat gaagtaccac cagtggactg	420
	gcctacaaag cacatagagt cctacaggct cgcattgcacc tcaactcgggg cggaaaaggt	480
55	tgagggtcttg cgtgccgctt tcaggctcgcg atatg	515

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5 <210> 837
 <211> 502
 <212> DNA
 <213> Staphylococcus aureus

10 <400> 837
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 atgatgtgtg tcatgtcaac agaggaagca gagttcagcc atgaatggac aaccggtgag 120
 tggaaagggtg aagtgaattt tgatagcgaa gagattctac tagattatgc atctcaggtg 180
 gaatcagatt ggccgcttac acatgggtcaa tttttctcta ttttgccgat ttatgattca 240
 15 ggtggatact tagagaaagt gtatcaaact gctaaatcgg tagaagccca aacgttccac 300
 gatgcgattt gtgcccttat cgtagaagag ctgtttgaat atgcaggcaa atggcgtaat 360
 attcgtgtgc aaggaccgac aacatttcta ccatacctga ctgtacaggt agcaatggca 420
 20 ggtgccatgt tgattggtct gcatcatcgc atctgttata cgacgagcgc ttcgggtctta 480
 actgaagcag ttaagcaatc ag 502

25 <210> 838
 <211> 452
 <212> DNA
 <213> Pseudomonas aeruginosa

30 <400> 838
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 tgacgtacag gaacagtact tgccaagcgt ttttagcgcaa gagtccgtca ctccatacat 120
 tgcaatgctg aatggagagc cgattgggta tgcccagtcg tacgttgctc ttggaagcgg 180
 35 ggacggatgg tgggaagaag aaaccgatcc aggagtacgc ggaatagacc agtcactggc 240
 gaatgcata caactgggca aaggcttggg aaccaagctg gttcgagcac tggttgagtt 300
 gctgttcaat gatccccgag tcaccaagat ccaaacggac ccgtcgccga gcaacttgcg 360
 40 agcgatccga tgctacgaga aagcgggggt tgagaggcaa ggtaccglaa ccaccccaga 420
 tggccagcc gtgtacatgg ttcaaacacg cc 452

45 <210> 839
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 <212> DNA
 <213> Escherichia coli

50 <400> 839
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 ggagcggatt tgctcaaagc gtggccgtca atggggcagc aacttggcgc tgttcacagc 180
 55 ctatcggttg atcaatgtcc gtttgagcgc aggtgtcgc gaatgttcgg acgcgccgtt 240

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	gatgtggtgt cccgcaatgc cgtcaatccc gacttcttac cggacgagga caagagtacg	300
5	ccgcagctcg atcttttggc tcgtgtcgaa cgagagctac cgggtcggct cgaccaagag	360
	cgcaccgata tggttgtttg ccatggtgat ccttgcacgc cgaacttcat ggtggaccct	420
	aaaactcttc aatgcacggg tctgatcgac cttgggcggc tcggaacagc agatcgctat	480
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	gagcgcgcct tcgctgtcct attca	565
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	aatgacggac agccggtata aagggaccac ctatgatgtg gaacgggaaa aggacatgat	180
25	gctatggctg gaaggaaagc tgctgttcc aaaggctctg cactttgaac ggcacatgatg	240
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	tgaacaaagc cctgaaaaga ttatcgagct gtatgcggag tgcacagggc tctttcactc	360
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	ttacttactg aataacgac tgcccgatgt ggattgcgaa aactgggaag aagacactcc	480
	atttaaagat ccgcgcgagc tgtatgattt tttaaagacg gaaaagcccg aagaggaact	540
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	tggctttatt gatcttggga gaagcggcag ggcggacaag tggatatgaca ttgccttctg	660
40	cgccgggtcg atcagggagg atatcgggga agaacagtat gtcgagc	707
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	aggacattca tcgcgcttgc tgcttcgag caagaagcgg ttgttggcgc tctcgcggct	180
	tacgtttctgc ccaagtttga gcaggcgcgt agtgagatct atatctatga tctcgcagtc	240
	tccggcgagc accgcgggca ggccattgcc accgcgctca tcaatctcct caagcatgag	300
55	gccaacgcgc ttggtgctta cgtgatcta	329

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<210> 842
 <211> 423
 <212> DNA
 5 <213> *Pseudomonas aeruginosa*

 <400> 842
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 gtccgtcact ccatacattg caatgctgaa tggagagccg attgggtatg ccagtcgta 180
 cgttgctctt ggaagcgggg acggatgggtg ggaagaagaa accgatccag gagtacgcgg 240
 15 aatagaccag tcaactggcg atgcatcaca actgggcaaa ggcttgggaa ccaagctggt 300
 tcgagcactg gttgagttgc tgttcaatga tcccagaggtc accaagatcc aaacggaccc 360
 gtcgccgagc aacttgcgag cgatccgatg ctacagaaaa gcgggggtttg agaggcaagg 420
 20 tac 423

 <210> 843
 <211> 613
 <212> DNA
 25 <213> *Staphylococcus aureus*

 <400> 843
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 tgataatttc aaagtagata gtattgaaat aatcggtagt ggttatgata gtgtggcata 180
 tttagttaat aatgaatata tttttaaaac aaaatttagt actaataaga aaaaaggtta 240
 35 tgcaaaagaa aaagcaatat ataatttttt aaatacaaat ttagaaacta atgtaaaaat 300
 tcctaataatt gaatattcgt atattagtga tgaattatct atactagggt ataaagaaat 360
 taaaggaact tttttaacac cagaaattta ttctactatg tcagaagaag aacaaaattt 420
 40 gttaaaacga gatattgcca gttttttaag acaaatgcac ggtttagatt atacagatat 480
 tagtgaatgt actattgata ataaacaaaa tgtattagaa gagtatatat tgttgctgta 540
 aactatztat aatgatttaa ctgatataga aaaagattat atagaaagtt ttatggaaaag 600
 45 actaaatgca aca 613

 <210> 844
 <211> 424
 <212> DNA
 50 <213> *Staphylococcus aureus*

 <400> 844
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 55 aggagtgaag ttgtcccttg gcaatatcct caaaaagag aatttatata cggtgagtgg 120

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	ctcaggggtg aatttgagaa tggacaaatt caggaaccaa gctatgatcc tgatttggtc	180
	attgttttag cacaagcaag aaagaatagt atttctctat ttggtcctga ttcttcaagt	240
5	atacttgctc ccgtacctt gacagatatt cgaagagcaa ttaaggattc ttgcccagaa	300
	ctaattgagg ggataaaagg tgatgagcgt aatgtaattt taaccctagc tcgaatgtgg	360
	caaacagtga ctactgggtga aattacctcg aaagatgtcg ctgcagaatg ggctatacct	420
10	cttt	424
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	<211> 532	
15	<212> DNA	
	<213> synthetic construct	
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	aggacatgat gctatggctg gaaggaaagc tgccctgttcc aaaggtcctg cactttgaac	180
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	ccgaattgga ttacttactg aataacgac tgcccgatgt ggattgcaa aactgggaag	420
30	aagacactcc atttaaagat ccgcgcgagc tgtatgattt tttaaagacg gaaaagcccg	480
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	<211> 200	
	<212> DNA	
	<213> Staphylococcus aureus	
	<400> 846	
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	attagtacag aggtgtaatt tcgtaactgc cattgaaata gaccataaat tatgcaaaac	180
45	tacagaaaat aaacttggtg	200
	<210> 847	
	<211> 510	
50	<212> DNA	
	<213> Enterococcus faecium	
	<400> 847	
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55	atagtataac ctcgaaactt gattcatcca actgggtgtt tgacgtagct ccgtacttga	120

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5	atattcctga tacgaaggct atgcttattt acgatgaaac agggcaatta gaaaattatt	300
	tatcagagat aagtgggtgca agaccaaata gacttactga agaaaatgct aattttttgt	360
	tgtgtaattt ctctaactta tgggtgatgg gaatcaacgt tctaaaaaga ggagaatatg	420
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	ctctatgaag cgccatattt aaaaagctac caagacgaag aggatgaaga ggatgaggag	180
25	gcagattgcc ttgaatatat tgacaatact gataaggtaa tatatct	227
30	<210> 849 <211> 708 <212> DNA <213> Staphylococcus aureus	
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	aaaaccagaa tctggaacgg ttgaaacgga tggcgaaatt caatattttg aacagcttaa	180
	catggatgtg gaaaatgatt ttaacacggt agacggtagt ttaatgagtg aactccatat	240
40	acctatgcat acaaccgaca gtatgagtgg tggtgaaaaa gcaaaatata aattagctaa	300
	tgtcatatca aattatagtc cgatattact tttagatgaa cctacaaatc acttggataa	360
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45	aagtcatgat agagcactta tagaccaaata tgctgacaca atttgggata tacaagaaga	480
	tggcacaata agagtgttta aaggtaatta cacacagtat caaaatcaat atgaacaaga	540
	acagttagaa caacaacgtc aatatgaaca gtatataagt gaaaaacaaa gattgtccca	600
50	agccagtaaa gctaaacgaa atcaagcgca acaaattggca caagcatcat caaaacaaaa	660
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<212> DNA
<213> Staphylococcus aureus

<400> 850
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gcaaaccocg aaggtggcaa ttacgttttt caaaatgaat ggttctcaga aactaattat 180
10 aaaggccgaa aaataccatg tattttcaaaa gaagctcaac ttctttttca ttctgggttat 240
gacttaacag aaaaagacc 259

<210> 851
<211> 544
<212> DNA
<213> Staphylococcus aureus

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55 gggthtacta ttaatgggtg agatggatat aaaaatgctc aaaaagtac caccactata 480

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	ctaattctgt tgttgtaaaa gatatagcgc catacatgtt agctggagga aatcctgcta	480
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	ctccgaccca tcaatggact ttatgggaca ccatcgtgta ttcgacgacg aaggattaga	300
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	caccgccagc cagttctgcg ctgatatccg ggcgccgacc gacgcatgaa tggcaatgcc	180
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55	ccacgcgcg agcagacctg caaggacgga gcagaacgcc gtcagcccga gcgttggcgc	480

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<213> Enterococcus faecium

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<210> 869

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<212> DNA

<213> Enterococcus faecium

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<211> 280

<212> DNA

<213> Enterococcus faecium

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 <213> *Enterococcus faecium*

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25

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 <213> *Enterococcus faecalis*

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	<211> 532	
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40	<213> Klebsiella oxytoca	
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45	ggagcaggat accgccggca ggccggagtt tctgactcgc ctgaatgaga tgcacgccgc	180
	cgaaccgcag atgcgtgaac aaactggggg gacgccggag atgattgatt tcattaccgc	240
	tgcttttgcc gaaagcaagc tggccatctg ggcgcgctat ctgaacgccg aagagctggc	300
50	ctttaccgcg cagcactatt tcgatcgct gatggagtgg ccggcgctgg tggccgacct	360
	gcatcgggcc tgtcgtgaga agcgagaccc ggccctcccc gaaggtcagc agctggcgca	420
	gcgctggctg gcgctgttcc agtcttacgc gggtaaagat gcgcagacgc agcagaagtt	480
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5 <210> 899
 <211> 500
 <212> DNA
 <213> *Klebsiella pneumoniae*

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 tctgtgatgg gcctgctttg gtcttttttg aaccctttat ttatgttaac agtatatact 180
 tttgtcttct ccgtgggtatt caaagccaga tgggtcaactg gtggggacga aagtaggaca 240
 15 cagtttgcta taatttttatt tgtcgggaatg atagtccatg gttttttaag tgaagtggta 300
 aataaagcgc cgttgattat tttgggaaat acaaactatg tgaagaaagt tatatttcca 360
 ttggaaacgc tgcctgttat ctctttatctt gcggcattat ttcatacttg taccagcctt 420
 20 tgtgtgttac tgatggcggt tttcattttt aatggatatt tacattggac catagtgttt 480
 ttacctttgg tctttttccc 500

25 <210> 900
 <211> 370
 <212> DNA
 <213> *Enterococcus faecium*

30 <400> 900
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 acaaacagag ttttcagaat cgcttggtccg tagtttgctg aatcacttag ggggttgctca 180
 35 ggaaactctg acgaaaccgt tatgtacatt aagtggggga gaagcgaccc gtctgacgat 240
 tgctttgctt tttactaagc caagtaatgt gttgctgtta gatgaaccga ctaattttat 300
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 40 gtttacctca 370

45 <210> 901
 <211> 400
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 gattatttac attctgccgt tagtcggaat tattgcctat cttgccgttg gcgagctcca 180
 tttaggcaaa cgccgcgctg agcgcgccag agcgatgtgg ccttccaccg caaatggct 240
 55 taacgacctt aaagcctgta agcatatctt cgccgaagaa aatagcagtg tcgctgcgcc 300

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	attattcaag ctttgcgagc gtcgtcaggg gatcgctggg gtcaaaggga atcagctaca	360
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	<211> 540	
	<212> DNA	
10	<213> Klebsiella pneumoniae	
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	gcattcagtt acatactgct aatgaagaaa ttggggaaaa acgttttggg actgcgcgtg	180
	ctattattaa aaatcttacc atctacaaat cagatggtag gactttgaca gagaaaccac	240
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	aggatgttgc tcttggcctt tccatatcca aagctcaggg aggggatatt tggggagata	360
	gtaatatggg cgcaggttca ccaattacac ttcgtccagg tagtcagcgt atcgtttata	420
25	aagcaacgct gcctataaat tcgggcgatt acctaataca ctgcggcctc gctatggttg	480
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	<212> DNA	
	<213> Klebsiella pneumoniae	
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	ttgataatgg tggttgtcag tgggcggcat cattgaatga acctaagggtg agctacatca	180
40	agtctcctta caactgtggg tttgggtgctg gacataatct tgcaataaaa gcaagtgcag	240
	actttgacgg ttattttctt atatgtaatc cggatataag ctttgataag cagtcacttg	300
	ataaattagt ttcgtttgcg tgggaaaatg agtatagttt tttgttttcc ccgcaaataa	360
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	taagacgttt ctttccagtg actgcaataa agtacgatgt taaatatgaa ctgaaagatg	480
	cagcctatga tgagatatct tccccaccaa cggatgtgtg ctggttcatg ttattaagta	540
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	tagatttatg tcgcccagca ttacagctaa ccaaaatata ctattatcct ggaacaacta	660
	ttgtccatgc ctttaataaa ggttcgtata aaagcaaatt attactttgg taccatattc	720
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<210> 904
 <211> 614
 <212> DNA
 5 <213> *Staphylococcus aureus*

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 gtggtatgag tgctgggtatg gtaatgccgg gtgtgacagg tttgattgca gatgtttcac 240
 15 caagccatca aaaagcaaaa aactttggct acatgtcagc gattatcaat tctggattca 300
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 20 aaaagtctac gacaagcggc ttccaaaaac ttgagcccca attattaaca aaaattaatt 480
 ggaaagtctt tattacgcca gcaattttta cgctcgtctt agcgttcggg ttatcggcat 540
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 25 cgattgcgat tacg 614

 <210> 905
 <211> 411
 <212> DNA
 30 <213> *Pseudomonas aeruginosa*

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 tgtattgaag cttatogacg aacaacgcgg gctgaacctg caggacctgg gacgccagat 180
 gtgccgcgac aaggcactga tcacccggaa gatccgcgag ctggagggaa gaaacctggg 240
 40 ccgccgcgag cgcaacccca gcgaccagcg cagcttccag ctcttcctca ccgacgaggg 300
 gctggccatc caccagcatg cggaggccat catgtcacgc gtgcatgacg agttgtttgc 360
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 <210> 906
 <211> 401
 <212> DNA
 50 <213> *Escherichia coli*

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 55 gatggagcca gcagtttggg gagctgaact tgctatgtca ctgtctggcc togagggtcg 180

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5	tggcgttggt gaagactggg aggggcatcc tgttgaatta ataaggggaa tgttggaattc	360
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20	tgagattttt gttggaggta ttgattttta aaataagaaa acatccatta aattaagcta	240
	tgtatcacia aaagcaaatg cctttaattc aggtttccca gcaagtgtta aagaagttgt	300
	tttaagcggg ttaacaaaga caaacgtct tttccaaaca tttaatatga aagataatga	360
25	aaaagtgatt aaagtactag aaagactgaa tataagtgat ttaattcata aaaatatagc	420
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	tatcgggtgtt gtagcagata ctgctactga agtagcatgt ttaaataagc atttgcattt	660
	ccatggtaca actgatgagt taaatcact tgatgaagtt gaaatttcaa aaatttatgg	720
35	acatcctgta cgttttgtcg at	742
40	<210> 908 <211> 352 <212> DNA <213> Staphylococcus aureus	
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	ataatcttaa atgatgggat gccgtagccg ttgaagattc aatgatatta gctacatcac	180
50	aaacacataa ctctccctct aaagacaaaa cataagcaat tttaactctt gtatcatctg	240
	atagagcctt aaaaactttc gctacatcca taggattctg tttagcaagg tcttttttag	300
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<212> DNA
<213> Enterococcus faecalis

<400> 909

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	atgttacaag gaaaaatgaa gttccggacc acccaaactt aattattgta cctccacgca	180
10	tgaaattata catgaagaaa aatcaagaaa ttaacaattt atataaccgc tttgtttcta	240
	atgaagatca ttctgtattc agtgtcgatg aatcgtttct tgatgtgact gcttcgctga	300
	cctattttta gtgtgacacc gcctataaac tggccaagat tattcaacgt gtgatttata	360
15	accatatggg attgtatgta acaatcggaa ttggggaaaa tccgttgctg gccaagttag	420
	cattggataa tgaagcaaag aatgcaccag gctttgtggc tgaatggcgc tatgaagatg	480
	tgccagaaaa agtttggcca atctcccctc ttacagaatt ttgtgggata ggaaatcgca	540
20	tggtgtctcg cttaaaaaag ctaggtattc ggtccattta tga	583

<210> 910
<211> 231
<212> DNA
<213> Candida albicans

<400> 910

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30	caaccagctt taaaatgtaa ttgttctaaa gcttcagtag aaaatgttgt tccatcatca	120
	aatgatgctt gtgcttggtg aaaaagaaat aaatcaagtt gtacttggtg tgctaagtct	180
35	atgtgtgatg gtactagaga tgggtgaaact gatttcacta acttgaaata a	231

<210> 911
<211> 240
<212> DNA
<213> Candida albicans

<400> 911

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45	agaatttagc cagaactttc actcatgatt ctttcaaaga tgactcgtca gcagggttat	180
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<210> 912
<211> 513
<212> DNA
<213> Candida albicans

<400> 912

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	ccaggatata tttattctaa aatctttttg gttgtttcag cagcattatt taatggattt	180
5	tcatttttca aagctaaaaa caacatgcaa ggtttacaaa atcaaagtgt ttcggtgttt	240
	atgtttttca ttccatttaa tactttgggtg caacaaatgt taccatactt tgtgaagcaa	300
	cgtgatgttt atgaagtgag agaagctcca tcaagaacat tcagttgggt tgcattttatt	360
10	gccggtcaaa ttacatcaga aattccttat caagttgccg ttggtaccat agcattttttc	420
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	<213> Candida albicans	
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	tggccaatcc caatcacctt agatgttgat gagaccactt ctaaaaaaca ttctgtttggt	300
30	gatagaattg tattaataga tttgagagat gaaactccat tggccatttt aactattgaa	360
	tctattttata aacctgataa aaaattagaa gcaaaaaaag tgttccgtgg tgatccagaa	420
	catcctgcta ataaatattt attagaaacc gctggcgatt attatatcgg tgggtgaatta	480
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	<213> Candida albicans	
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	ccattaccac aaatattcag gtgacatagg gcctgccttt ttaaccagat ttaatccgac	300
55	aggagcagaa ccgatccctc agaacttttt gttcaatgaa acaagaaatg ccacttgga	360

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5 ggtcgaacct ggaaaaactt actttgttag gattcttaat gttggtggtt ttgtatcaca 420
 gtacttggtg atggaagatc atgaatttac tattgttgag atcgatggcg tttacgttga 480
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 <213> Candida albicans

 15 <400> 915
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 25 cccaatocca gttattgttg gtataatttg tgggtcttgc gtgggtgcct tgttgtacta 480
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 35 <210> 916
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 <212> DNA
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 40 <400> 916
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 45 gatctaagaa aattgtcaag tttattgaaa agcaagataa agctgaccgt caacgtatat 600
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50 <210> 919
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 <212> DNA
 <213> Glycine max

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Claims

1. A DNA microarray for direct identification and characterisation of microorganisms in a sample or clinical specimen, wherein the microarray comprises gene probes being derived from DNA sequences or partial DNA sequences of the microorganisms to be identified or DNA sequences complementary or homologous thereto, and having a length of at least 100 nucleotides (nt).

2. The DNA microarray of claim 1, wherein

- (i) the length of the gene probes is from 100 to 1000 nt, preferably from 200 to 800 nt; and/or
- (ii) the gene probes are specific for a specific microbial species or group of microorganisms to be identified and preferably are DNA sequences selected from the groups consisting of (a) species specific gene probes, (b) virulence gene probes and (c) resistance gene probes; and/or
- (iii) the microorganisms to be detected are microorganisms which cause bacteremia, fungemia or sepsis and include bacteria and fungi, preferably the microorganisms are selected from the group consisting of *Candida albicans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Proteus vulgaris*, *Enterobacter cloacae*, *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, *Acinetobacter baumannii*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus lugdunensis*, *Staphylococcus warneri*, *Streptococcus agalactiae*, *Streptococcus bovis*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, most preferably are *S. aureus*, *E. coli* and/or *P. aeruginosa*; and/or
- (iv) the sample is selected from whole blood, serum, urine, saliva, liquor, sputum, punctate, stool, pus, wound fluid, positive blood cultures, preferably is positive blood cultures; and/or
- (v) the array further comprises DNA sequences selected from the group (d) consisting of control gene probes coding for negative controls and positive controls.

3. The DNA microarray of claim 2, which is suitable for identification of bacteremia, fungemia or sepsis and wherein the set of gene probes preferably comprises gene probes selected from

(a) species specific gene probes for

- (i) *Staphylococcus aureus* including gene probes derived from *cataSaur*, *clfA*, *clfB*, *coa*, *l-clpC*, *l-clpP*, *l-ctaA*, *l-ctsR*, *l-dltA*, *l-dltB*, *l-dltC*, *l-dnaK*, *l-eltK*, *l-femD*, *l-glnA*, *l-glnR*, *l-grlA*, *l-grlB*, *l-groEL*, *l-groES*, *l-hemA*, *l-hemE*, *l-hemH*, *l-hemL*, *l-hemY*, *l-lepA*, *l-lrgA*, *l-lrgB*, *l-lytM*, *l-menB*, *l-menD*, *l-menE*, *l-menF*, *l-mreB*, *l-mreR*, *l-mutL*, *l-mutS*, *l-NAG*, *l-pbg*, *l-pbpF*, *l-pdhB*, *l-pdhC*, *l-rsbU*, *l-rsbV*, *l-rsbW*, *l-sgp*, *l-sirR*, *l-sodA*, *l-sodB*, *l-sstA*, *l-sstB*, *l-sstC*, *l-sstD*, *l-trx*, *l-yhiN*, *epiP-bsaP*, *geh*, *gyrA*, *gyrB*, *hemB*, *hemC*, *hemD*, *hemN*, *hsdS*, *hsdS*, *lip*, *menC*, *nuc*, *pdhD*, *rpoB*, *SAV0431*, *SAV0439*, *SAV0440*, *SAV0441*, *sigB*, *spa*, *sstC*, *tag*, *tyrA*, *l-aroC*, *l-aroA*, *l-cna*, *l-ebpS*, *l-eno*, *l-fbpA*, *l-fib*, *l-fnbB*, *l-srtA*, *l-stpC*, *l-fnbA*, *l-spa*, *l-aroE*, *l-aroF*, *l-aroG*, *l-aspx23*, *l-atl*;
- (ii) *Escherichia coli* including gene probes derived from *b1169*, *envZ*, *fliCb*, *nfrB*, *nlpA*, *pilAe*, *yach*, *yagX*, *ycdS*, *yciQ*, *ymcA*;
- (iii) *Staphylococcus epidermidis* including gene probes derived from *ardeSE0106*, *ardeSE0107*, *aroSE0105*, *atlE*, *agrB*, *agrC*, *alphSE1368*, *gad*, *glucSE1191*, *hsp10*, *icaA*, *icaB*, *mvaSSepid*, *nitreSE1972*, *nitreSE1974*, *nitreSE1975*, *oiamtSE1209*, *ORFISepid*, *ORF3bSepid*, *qacR*, *sin*, *ureSE1861*, *ureSE1863*, *ureSE1864*, *ureSE1865*, *ureSE1867*;
- (iv) *Staphylococcus haemolyticus* including gene probes derived from *folQShaemolyt*, *m vaCShaem olyticus*, *mvaDShaemolyt*, *mvaK1Shaemolyticus*, *m vaSShaem olyticus*, *RNApolsigm*;
- (v) *Staphylococcus lugdunensis* including gene probes derived from *agrB2Stalugd*, *agrC2Stalugd*, *agrC-Stalugd*, *slam Stalugd*;
- (vi) *Staphylococcus warneri* including gene probes derived from *msrw1Stwar*, *nukMStwar*, *proDStwar*, *proMStwar*, *sigrpoStwar*, *tnpStwar*;
- (vii) *Candida albicans* including gene probes derived from *ARG56*, *ASL43f*, *BGL2*, *CACHS3*, *CCT8*, *CDC37*, *CEF3*, *CHS1*, *CHS2*, *CHS4*, *CHS5*, *CHT1*, *CHT2*, *CHT4*, *CSA1*, *5triphosphatase*, *AAF1*, *ADH1*, *ALS1*, *ALS7*, *EDT1*, *ELF*, *ESS1*, *FAL1*, *GAP1*, *GNA1*, *GSC1*, *GSL1*, *HIS1*, *HTS1*, *HWP1*, *HYR1*, *INT1a*, *KRE15f*, *KRE6*, *KRE9*, *MIG1*, *MLS1*, *MP65*, *NDE1*, *PFK2*, *PHR1*, *PHR2*, *PHR3*, *PRR1*, *PRS1*, *RBT1*, *RBT4*, *RHO1*, *RNR1*, *RPB7*, *RPL13*, *RVS167*, *SHA3*, *SKN1*, *SRB1*, *TCA1*, *TRP1*, *YAE1*, *YRB1*, *YST1exon2*;
- (viii) *Enterococcus faecalis* including gene probes derived from *arcA*, *arcC*, *bkdA*, *cad*, *camE1*, *csrA*, *dacA*,

dfr, *dhoD1a*, *ABC-eltA*, *agrBfs*, *agrCfs*, *dnaE*, *ebsA*, *ebsB*, *eep*, *efaR*, *gls24_glsB*, *gph*, *gyrAEf*, *metEf*, *mntHCb2*, *mob2*, *mvaD*, *mvaE*, *parC*, *pcfG*, *phoZ*, *polC*, *ptb*, *recS1*, *rpoN*, *tms*, *tyrDC*, *tyrS*;

(ix) *Enterococcus faecium* including gene probes derived from *bglB*, *bglR*, *bglS*, *efmA*, *efmB*, *efmC*, *mreC*, *mreD*, *mvaDEfaecium*, *mvaEEfaecium*, *mvaK1Efaecium*, *mvaK2Efaecium*, *mvaSEfaecium*, *orf3_4Efaeciumb*, *orf6_7Efaecium*, *orf7_8Efaecium*, *orf9_10Efaecium*;

(x) *Klebsiella pneumonia* including gene probes derived from *atsA*, *atsB*, *budC*, *citA*, *citW*, *citX*, *dalD*, *dalk*, *dalT*, *acoA*, *acoB*, *acoC*, *ahlK*, *fimK*, *glfKPN2*, *ltrA*, *mdcC*, *mdcF*, *mdcH*, *mrkA*, *mtrK*, *nifF*, *nifK*, *nifN*, *tyrP*, *ureA*, *wbbO*, *wza*, *wzb*, *wzmKPN2*, *wztKPN2*, *yohH*, *liac*;

(xi) *Klebsiella oxytoca* including gene probes derived from *cymA*, *cymD*, *cymE*, *cymH*, *cymI*, *cymJ*, *ddrA*, *fdt-1*, *fdt-2*, *fdt-3*, *gatY*, *hydH*, *masA*, *nasA*, *nasE*, *nasF*, *pehX*, *pelX*, *tagH*, *tagK*, *tagT*;

(xii) *Pseudomonas aeruginosa* including gene probes derived from *glpR*, *lasRb*, *OrfX*, *pa0260*, *pa0572*, *pa0625*, *pa0636*, *pa1046*, *pa1069*, *pa1846*, *pa3866*, *pa4082*, *pilAp*, *PilAp2*, *pilC*, *PstP*, *purK*, *uvrDII*, *vsml*, *vsmR*, *xcpX*;

(xiii) *Streptococcus pneumoniae* including gene probes derived from *cap1EStrepneu*, *cap1FStrepneu*, *cap1GStrepneu*, *cap3AStrepneu*, *cap3BStrepneu*, *celAStrepneu*, *celBStrepneu*, *cglAStrepneu*, *cglBStrepneu*, *cglCStrepneu*, *cglDStrepneu*, *cinA*, *cps14EStrepneu*, *cps14FStrepneu*, *cps14GStrepneu*, *cps14H-Strepneu*, *cps19aHStrepneu*, *cps19aIStrepneu*, *cps19aKStrepneu*, *cps19f-GStrepneu*, *cps23fGStrepneu*, *dexB*, *dinF*, *1760Strepneu*, *acyPStrepneu*, *endAStrepneu*, *exoAStrepneu*, *exp72*, *fnlAStrepneu*, *fnlBStrepneu*, *fnlCStrepneu*, *gct18Strepneu*, *hexB1*, *hftsHstrepneu*, *immunofrag1Strepneu*, *immunofrag-2Strepneu*, *immunofrag3Strepneu*, *kdtBStrepneu*, *lysAStrepneu*, *pcpBStrepneu*, *pflCStrepneu*, *plpA*, *prtA1Strepneu*, *pspC1Strepneu*, *pspC2*, *purRStrepneu*, *pyrDAStrepneu*, *SP0828Strepneu*, *SP0830Strepneu*, *SP0833Strepneu*, *SP0837_38-Strepneu*, *SP0839Strepneu*, *ugdStrepneu*, *uncC*, *vicXStrepneu*, *wchA6bStrepneu*, *wci4Strepneu*, *wciK4Strepneu*, *wciL4Strepneu*, *wciN6bStrepneu*, *wciO6b-Strepneu*, *wciP6bStrepneu*, *wciY18Strepneu*, *wzdbStrepneu*, *wze6b-Strepneu*, *wzy18Strepneu*, *wzy4Strepneu*, *wzy6bStrepneu*, *xpt*;

(xiv) *Streptococcus agalactiae* including gene probes derived from *cpsA1Strgal*, *cpsB1Strgal*, *cpsC1Strgal*, *cpsD1Strgal*, *cpsE1Strgal*, *cpsG1Strgal*, *cpsIStrgal*, *cpsJStrgal*, *cpsKStrgal*, *cpsMStrgal*, *cpsYStrgal*, *cylBStraga*, *cylEStraga*, *cylFStraga*, *cylHStraga*, *cylIStraga*, *cylJStraga*, *cylKStraga*, *0487Straga*, *0488Straga*, *0493Straga*, *0495Straga*, *0498Straga*, *0500Straga*, *0502Straga*, *0504Straga*, *folDStraga*, *neuA1Strgal*, *neuB1Strgal*, *neuC1Strgal*, *neuD1Strgal*, *recNStraga*, *ileSStraga*;

(xv) *Streptococcus pyogenes* including gene probes derived from *cyclStrpyog*, *fah_rph_hlo_Strpyog*, *int*, *int315.5*, *murEStrpyog*, *oppA*, *oppCStrpyog*, *oppD*, *SPy0382Strpyog*, *SPy0390Strpyog*, *SPyM3_1351*, *vicXStrpyog*;

(xvi) *Streptococcus viridans* including gene probes derived from *573Strpmut*, *580SStrpmut*, *581_582SStrpmut*, *584SStrpmut*, *dltAStrmut*, *dltBStrmut*, *dltCpx1Strmut*, *dltDStrmut*, *lichStrbov*, *lytRStprmut*, *lytSStrpmut*, *pepQStrmut*, *pflCStrmut*, *recNStprmut*, *ytqBStrmut*;

(xvii) *Proteus mirabilis* including gene probes derived from *atfA*, *atfB*, *atfC*, *ccmPrmi1*, *cyaPrmi*, *aad*, *flfB*, *flfD*, *flfN*, *flhD*, *floA*, *ftsK*, *gstB*, *hemCPrmi*, *hemDPrmi*, *hev*, *katA*, *lpp1*, *menE*, *mfd*, *nrpA*, *nrpB*, *nrpG*, *nrpS*, *nrpT*, *nrpU*, *pat*, *pmfA*, *pmfC*, *pmfE*, *ppaA*, *rsbA*, *rsbC*, *speB*, *stmA*, *stmB*, *terA*, *terD*, *umoA*, *umoB*, *umoC*, *ureR*, *xerC*, *ygbA*;

(xviii) *Proteus vulgaris* including gene probes derived from *envZPrvu*, *frdC*, *frdD*, *infBPrvu*, *lad*, *tna2*; and/or

(b) virulence gene probes for

(i) *Staphylococcus aureus* including gene probes derived from *bsaE*, *bsaG*, *cap5h*, *cap5i*, *cap5j*, *cap5k*, *cap8H*, *cap8I*, *capBJ*, *cap8K*, *I-hld*, *I-hysA*, *I-IgGbg*, *EDIN*, *eta*, *etb*, *hglA*, *hglB*, *hglC*, *hla*, *hlyA*, *hlyB*, *lukF*, *lukS*, *NAG*, *sak*, *sea*, *seb*, *sec1*, *seg*, *seh*, *sel*, *set15*, *set6*, *set7*, *set8*, *sprV8*, *tst*, *I-sdrC*, *I-sdrD*, *I-sdrE*;

(ii) *Escherichia coli* including gene probes derived from *b1202*, *eae*, *eltB*, *escR*, *escT*, *escU*, *espB*, *fes*, *fteA*, *hlyA*, *hlyB*, *iucA*, *iucB*, *iucC*, *papG*, *rfaE*, *shuA*, *SLTII*, *toxA-LTPA*, *VT2vaB*;

(iii) *Staphylococcus epidermidis* including gene probes derived from *gcaD*, *hld_orf5*, *icaC*, *icaD*, *icaR*, *psm_beta1and2*, *purR*, *spoVG*, *yabJ*;

(iv) *Staphylococcus haemolyticus* including gene probes derived from *lipShaemolyt*;

(v) *Staphylococcus lugdunensis* including gene probes derived from *fbIStalugd*, *slushABCStalugd*;

(vi) *Staphylococcus warneri* including gene probes derived from *gehASTwar*;

(vii) *Candida albicans* including gene probes derived from *CCN1*, *CDC28*, *CLN2*, *CPH1*, *CYB1*, *EFG1*, *MNT1*, *RBF1*, *RBF1*, *RIM101*, *RIM8*, *SEC14*, *SEC4*, *TUP1*, *YPT1*, *ZNF1*, *CZF1*;

(viii) *Enterococcus faecalis* including gene probes derived from *asa1*, *asp1*, *cgh*, *cylA*, *cylB*, *cylI*, *cylL*, *cylS*, *cylM*, *ace*, *ef00108*, *ef00109*, *ef0011*, *ef00113*, *ef0012*, *ef0022*, *ef0031*, *ef0032*, *ef0040*, *ef0058*,

entA, *esa*, *esp*, *gelE*, *groEL*, *groES*, *rt1*, *sala*, *salb*, *sea1*, *sep1*, *vick*, *yycH*, *yycl*, *yycJ*;

(ix) *Enterococcus faecium* including gene probes derived from *entA_entl*, *entD*, *entR*, *oep*, *sagA*;

(x) *Klebsiella pneumonia* including gene probes derived from *cim*, *aldA*, *hemly*, *pSL017*, *pSL020*, *rcaA*, *rmlC*, *rmlD*, *waaG*, *wbbD*, *wbbM*, *wbbN*, *wbdA*, *wbdC*, *wztKpn*, *yibD*;

(xi) *P. aeruginosa* including gene probes derived from *aprA*, *aprE*, *ctx*, *algB*, *algN*, *algR*, *ExoS*, *fpvA*, *lasRa*, *lipA*, *lipH*, *Orf159*, *Orf252*, *pchG*, *PhzA*, *PhzB*, *PLC*, *plcN*, *plcR*, *pvdD*, *pvdF*, *pyocinS1*, *pyocinS1im*, *pyocinS2*, *pys2*, *rbf303*, *rhlA*, *rhlB*, *rhlR*, *TnAP41*, *toxA*;

(xii) *Streptococcus pneumoniae* including gene probes derived from *igaStrpneu*, *lytA*, *nanA*, *nanBStrpneu*, *pcpCStrpneu*, *ply*, *prtAStrpneu*, *pspA*, *SP0834Strpneu*, *sphtraStrpneu*, *wciJStrpneu*, *wziyStrpneu*, *wzxStrpneu*;

(xiii) *Streptococcus agalactiae* including gene probes derived from *CAMPfactor*, *0499Straga*, *hylStragal*, *lipStragal*;

(xiv) *Streptococcus pyogenes* including gene probes derived from *DNaseIStrpyog*, *fba2Strpyog*, *fhuAS-trpyog*, *fhuB1Strpyog*, *fhuDStrpyog*, *fhuGStrpyog*, *hylA*, *hylP*, *hylp2*, *oppB*, *ropB*, *scpAStrpyog*, *sloStrpyog*, *smexZStrpyog*, *sof*, *speA*, *speB2Strpyog*, *speCStrpyog*, *speJStrpyog*, *srtBStrpyog*, *srtCStrpyog*, *srtEStrpyog*, *srtFStrpyog*, *srtGStrpyog*, *srtIStrpyog*, *srtKStrpyog*, *srtRStrpyog*, *srtTStrpyog*, *vickStrpyog*;

(xvi) *Streptococcus viridans* including gene probes derived from *hlyXStrmut*, *igaStrmitis*, *igaStrsanguis*, *perMStrmut*;

(xvii) *Proteus mirabilis* including gene probes derived from *flaA*, *laD*, *fliA*, *hpmA*, *hpmB*, *lpsPrmi*, *mrpA*, *mrpB*, *mrpC*, *mrpD*, *mrpE*, *mrpF*, *mrpG*, *mrpH*, *mrpI*, *mrpJ*, *patA*, *putA*, *uca*, *ureDPrmi*, *ureEPrmi*, *ureFPrmi*, *zapA*, *zapB*, *zapD*, *zapE*; and/or

(c) resistance gene probes derived from genes coding for

(i) beta-lactams resistance including gene probes derived from *blaIMP-7*, *meclSepid*, *blaOXA-10*, *blaB*, *ampC*, *I-blaR*, *blaOXA-32*, *bla-CTX-M-22*, *bbp2aStrpneu*, *blaSHV-1*, *blaOXA-2*, *blaRShaemolyt*, *blaIMP-7*, *I-mecR*, *blaOXY*, *dacCStrpyog*, *femA*, *mecA*, *blaShaemolyt*, *blavim*, *bbp2b*, *bbp2prim*, *eSepid*, *bbp2x*, *bbp3Saureuc*, *bbp4*, *bbp5Efaecium*, *bbpC*, *I-mecI*, *bbp1a*, *I-blaI*, *blaTEM-106*, *blaOXY-KLOX*, *ftsWEF*, *fmhB*, *cumA*, *femBShaemolyt*, *blaPER-1*, *bla_FOX-3*, *blaA*, *psrb*, *fmhA*, *mecR1Sepid*, *blaZ*, *blaOXA-1*, *fox-6*, *blaPrmi*;

(ii) aminoglycosides resistance including gene probes derived from *aacA_aphDStwar*, *aacC1*, *aacC2*, *strB*, *aadA*, *aadB*, *aadD*, *aacA4*, *strA*, *aph-A3*, *aacC1*, *aacA4*, *aacA-aphD*, *I-spc*, *aphA3*;

(iii) macrolides-lincosamides-streptogramins resistance including gene probes derived from *ermC*, *linB*, *satSA*, *mdrSA*, *I-linA*, *ermB*, *ermA*, *satA*, *msrA*, *mphBM*, *mefA*, *mrx*;

(iv) trimethoprim resistance including gene probes derived from *dfrA*, *dfrStrpneu*;

(v) chloramphenicol resistance including gene probes derived from *cat*, *catEfaecium*, *cmlA5*;

(vi) tetracyclines resistance including gene probes derived from *tetAJ*, *tetL*, *tetM*

(vii) glycopeptides resistance including gene probes derived from *vanH(tn)*, *vanA*, *vanHB2*, *vanR*, *vanRB2*, *vanS(tn)*, *vanSB2*, *vanVIB2*, *ddl*, *ble*, *vanXB2*, *vanY(tn)*, *vanYB2*, *vanB*, *vanZ(tn)*, *vanC-2*, *vanX(tn)*;

(viii) multiple target resistance including gene probes derived from *acrB*, *m exB*, *I-qacA*, *sull*, *sul*, *cadB-Stalugd*, *mexA*, *acrR*, *emeA*, *acrA*, *rtn*, *abcXStrmut*, *qacEdelta1*, *elkT-abcA*, *I-cadA*, *alba*, *wzm*, *msrCb*, *nov*, *wzt*, *wbbI*, *norA23*, *mexR*, *arr2*, *mreA*, *I-cadC*, *uvrA*;

(ix) fungicide resistance, especially *C. albicans* fungicide resistance, including gene probes derived from *CRD2*, *CDR1*, *MET3*, *FET3*, *FTR2*, *MDR1-7*, *ERG11*, *SEC20*.

4. The DNA microarray of claim 2 or 3, wherein

(i) the array comprises the minimal number of species specific gene probes of group (a) which is sufficient for species identification, preferably the array comprises at least 2 different gene probes per target species of group (a); and/or

(ii) the array comprises the minimal number of virulence gene probes of group (b) sufficient for virulence determination, preferably at least 1 gene probe, more preferably at least 5 different gene probes per target species of group (b); and/or

(iii) the array comprises the minimal number of resistance gene probes of group (c) sufficient for determination of resistance, preferably at least 1 gene probe, more preferably at least 5 different gene probes of group (c); and/or

(iv) the DNA sequences are selected from the group consisting of SEQ ID NOs 1-918, complementary sequences thereto, addition mutants, deletion mutants, substitution mutants and homologues thereof.

5. The DNA microarray of claim 4, wherein

(i) the gene probes of group (a) are selected from SEQ ID NO: 1-99, 142-152, 174-199, 209-214, 216-219, 222-229, 231-291, 308-342, 377-393, 399-431, 449-490, 523-591, 606-639, 645-656, 687-701, 706-749 and 776-781;

(ii) the gene probes of group (b) are selected from SEQ ID NO: 100-141, 153-173, 200-208, 215, 220-221, 230, 292-307, 343-376, 394-398, 432-448, 491-522, 592-605, 640-644, 657-686, 702-705, 750-775 and 782-784; and/or

(iii) the gene probes of group (c) are selected from SEQ ID NO:785-918, preferably from SEQ ID NO:785-882.

6. The DNA microarray of claim 4 or 5, which

(I) is suitable for identification of *Staphylococcus aureus* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:1-99, preferably comprises at least the gene probes represented by SEQ ID NO:71 and 68; and/or

(II) is suitable for identification of *Escherichia coli* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:142-152, preferably at least the gene probes represented by SEQ ID NO:143 and 149; and/or

(III) is suitable for identification of *Staphylococcus epidermidis* and comprises gene probes of group (a) selected from SEQ ID NO:174-199, preferably at least the gene probes represented by SEQ ID NO:177 and 184; and/or

(IV) is suitable for identification of *Staphylococcus haemolyticus* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:209-214, preferably at least the gene probes represented by SEQ ID NO:209 and 210; and/or

(V) is suitable for identification of *Staphylococcus lugdunensis* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:216-219, preferably at least the gene probes represented by SEQ ID NO:216 and 219; and/or

(VI) is suitable for identification of *Staphylococcus warneri* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO: 224-229, preferably at least the gene probes represented by SEQ ID NO: 224 and 225; and/or

(VII) is suitable for identification of *Candida albicans* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:231-291, preferably at least the gene probes represented by SEQ ID NO: 231 and 232; and/or

(VIII) is suitable for identification of *Enterococcus faecalis* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:308-342, preferably at least the gene probes represented by SEQ ID NO:308 and 310; and/or

(IX) is suitable for identification of *Enterococcus faecium* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:377-393, preferably at least the gene probes represented by SEQ ID NO:377 and 380; and/or

(X) is suitable for identification of *Klebsiella pneumonia* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:399-431, preferably at least the gene probes represented by SEQ ID NO:399 and 402; and/or

(XI) is suitable for identification of *Klebsiella oxytoca* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:449-469, preferably at least the gene probes represented by SEQ ID NO: 449 and 455; and/or

(XII) is suitable for identification of *Pseudomonas aeruginosa* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:470-490, preferably at least the gene probes represented by SEQ ID NO:470 and 471; and/or

(XIII) is suitable for identification of *Streptococcus pneumoniae* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:523-591, preferably at least the gene probes represented by SEQ ID NO:523 and 524; and/or

(XIV) is suitable for identification of *Streptococcus agalactiae* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:606-639, preferably at least the gene probes represented by SEQ ID NO:606 and 619; and/or

(XV) is suitable for identification of *Streptococcus pyogenes* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:645-656, preferably at least the gene probes represented by SEQ ID NO:645 and 646; and/or

(XVI) is suitable for identification of *Streptococcus viridans* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:687-701, preferably at least the gene probes represented by SEQ ID

NO:687 and 691 ; and/or

(XVII) is suitable for identification of *Proteus mirabilis* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:706-749, preferably at least the gene probes represented by SEQ ID NO: 706 and 710; and/or

(XVIII) is suitable for identification of *Proteus vulgaris* and comprises one or more or all of the gene probes of group (a) selected from SEQ ID NO:776-781, preferably at least the gene probes represented by SEQ ID NO: 776 and 777.

7. The DNA microarray of claim 6, which further comprises

(I) for the characterisation of *Staphylococcus aureus*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:100-141, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(II) for the characterisation of *Escherichia coli*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:153-173, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(III) for the characterisation of *Staphylococcus epidermidis*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:200-208, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(IV) for the characterisation of *Staphylococcus haemolyticus*: one or more or all of the gene probe of group (b) represented by SEQ ID NO:215, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(V) for the characterisation of *Staphylococcus lugdunensis*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:220-221, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(VI) for the characterisation of *Staphylococcus warneri*: one or more or all of the gene probe of group (b) represented by SEQ ID NO:230, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(VII) for the characterisation of *Candida albicans*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:292-307, and/or of the gene probes of group (c) selected from SEQ ID NO:910-918; and/or

(VIII) for the characterisation of *Enterococcus faecalis*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:343-376, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(IX) for the characterisation of *Enterococcus faecium*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:394-398, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(X) for the characterisation of *Klebsiella pneumoniae*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:432-448, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XI) for the characterisation of *Klebsiella oxytoca*: one or more or all of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XII) for the characterisation of *Pseudomonas aeruginosa*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:491-522, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XIII) for the characterisation of *Streptococcus pneumoniae*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:592-605, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XIV) for the characterisation of *Streptococcus agalactiae*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:640-644, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XV) for the characterisation of *Streptococcus pyogenes*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:657-686, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XVI) for the characterisation of *Streptococcus viridans*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:702-705, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XVII) for the characterisation of *Proteus mirabilis*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:750-775, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909; and/or

(XVIII) for the characterisation of *Proteus vulgaris*: one or more or all of the gene probes of group (b) selected from SEQ ID NO:782-784, and/or of the gene probes of group (c) selected from SEQ ID NO:785-909.

8. Use of the DNA microarray of any of claims 1 - 7 for *in vitro* identification and characterisation of microorganisms

in a sample or in a clinical specimen, preferably for the diagnosis of bacteremia or sepsis.

9. An *in vitro* method for identification and characterisation of microorganisms in a sample or in a clinical specimen comprising

- (a) isolating the total DNA from the sample or clinical specimen and labelling the DNA with a reporter molecule;
- (b) applying the DNA thus obtained to the DNA microarray of anyone of claims 1-7 and hybridising the DNA with the gene probes of the DNA microarray; and
- (c) detecting DNA bound to the DNA microarray by determination of the amount of the reporter molecules bound to the array.

10. The method of claim 9,

- (i) which is a method for diagnosis of bacteremia, fungemia or sepsis; and/or
- (ii) wherein the clinical specimen is a positive blood culture; and/or
- (iii) wherein the ratio of microbial DNA to total DNA isolated from said sample or clinical specimen is less than 100 %, preferably from 1% to 99%; and/or
- (iv) wherein the reporter molecule is a fluorochrome; and/or
- (v) wherein the determination of the amount of reporter molecules bound to the array is achieved by visualization of the reporter molecule; and/or
- (vi) wherein the DNA isolated in step (a) is labelled and applied to the DNA microarray without prior amplification.

11. A kit for detection of microorganisms in a sample or clinical specimen comprising the microarray of anyone of claims 1 to 7.

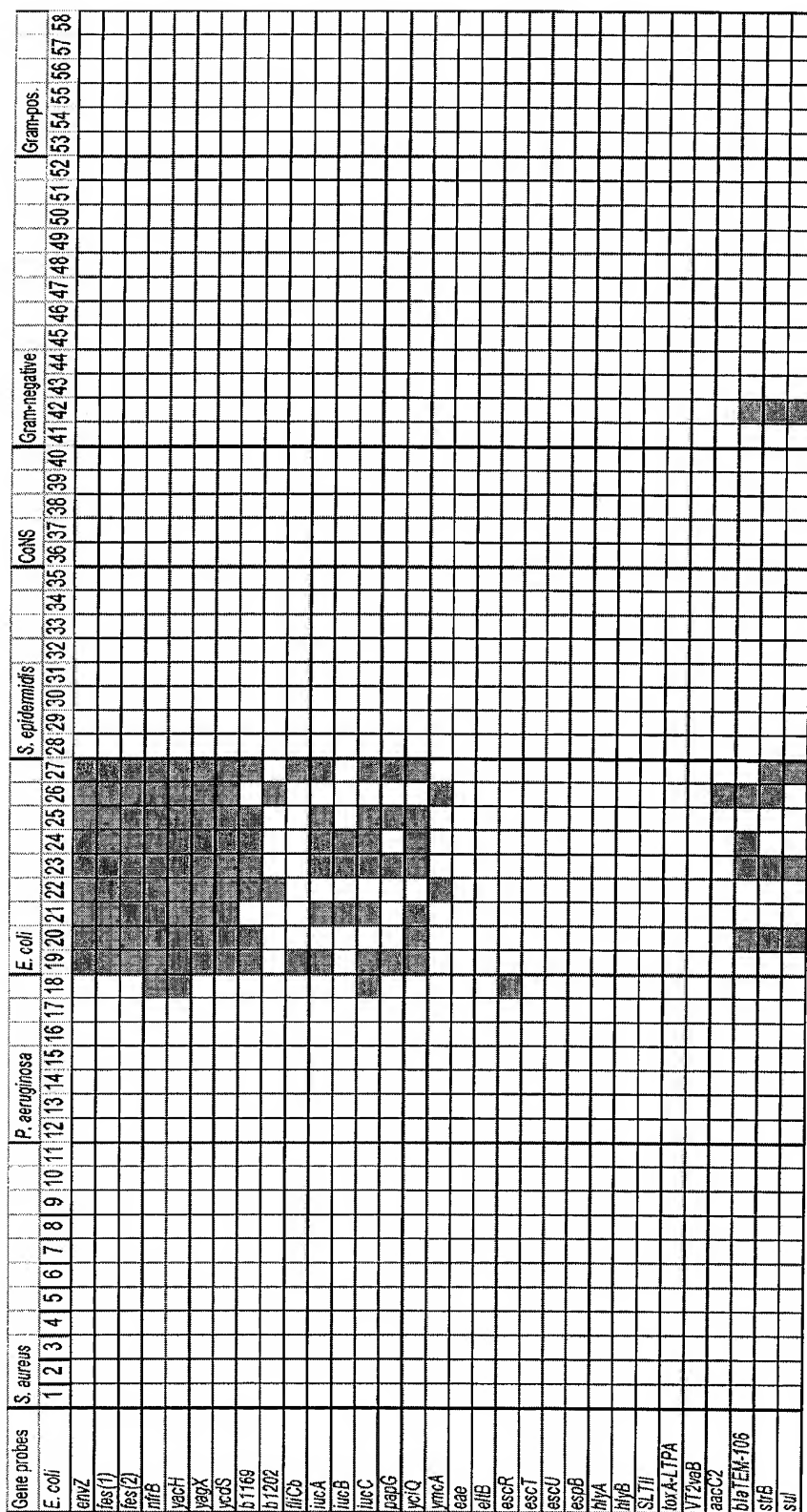
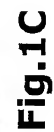


Fig. 1A





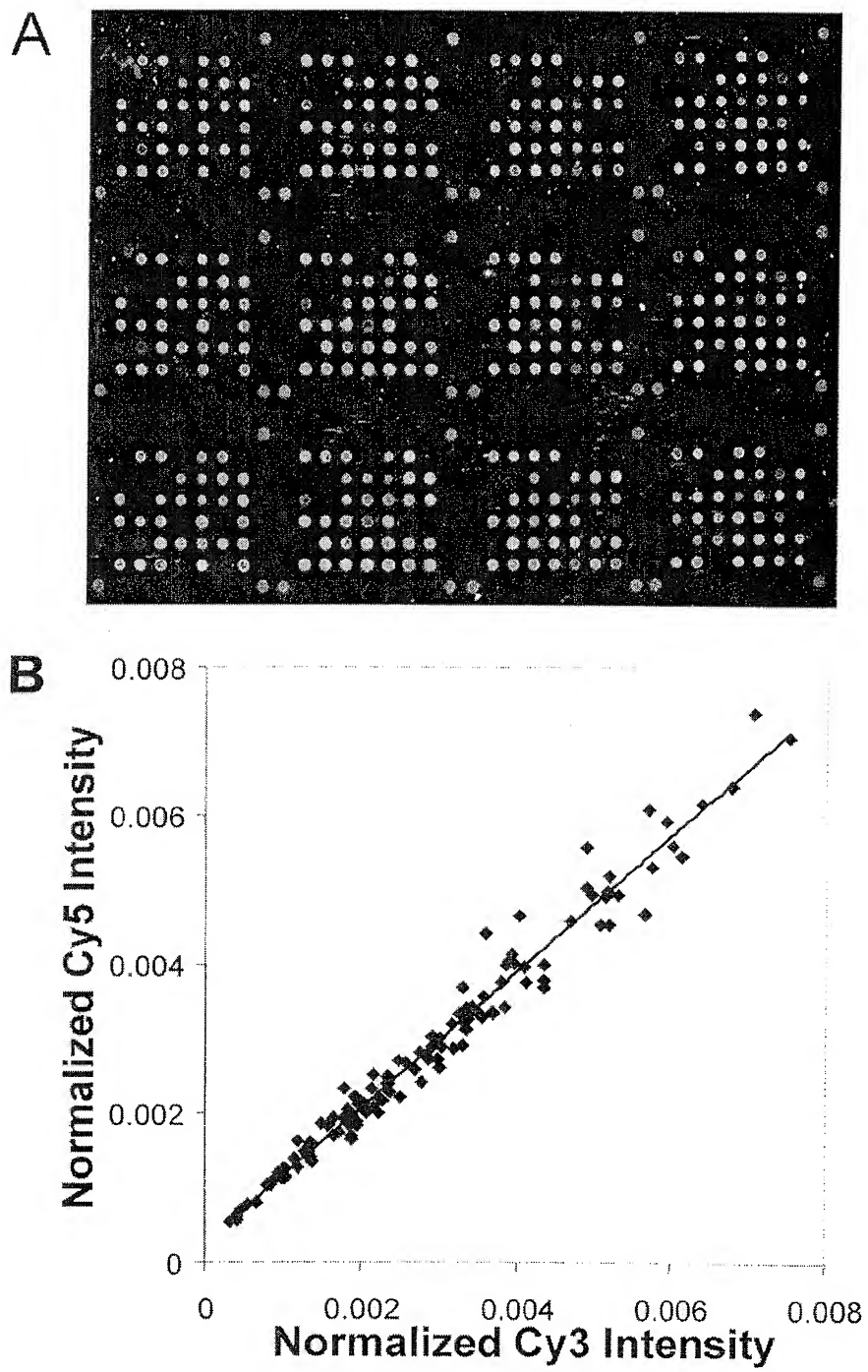


Fig.2

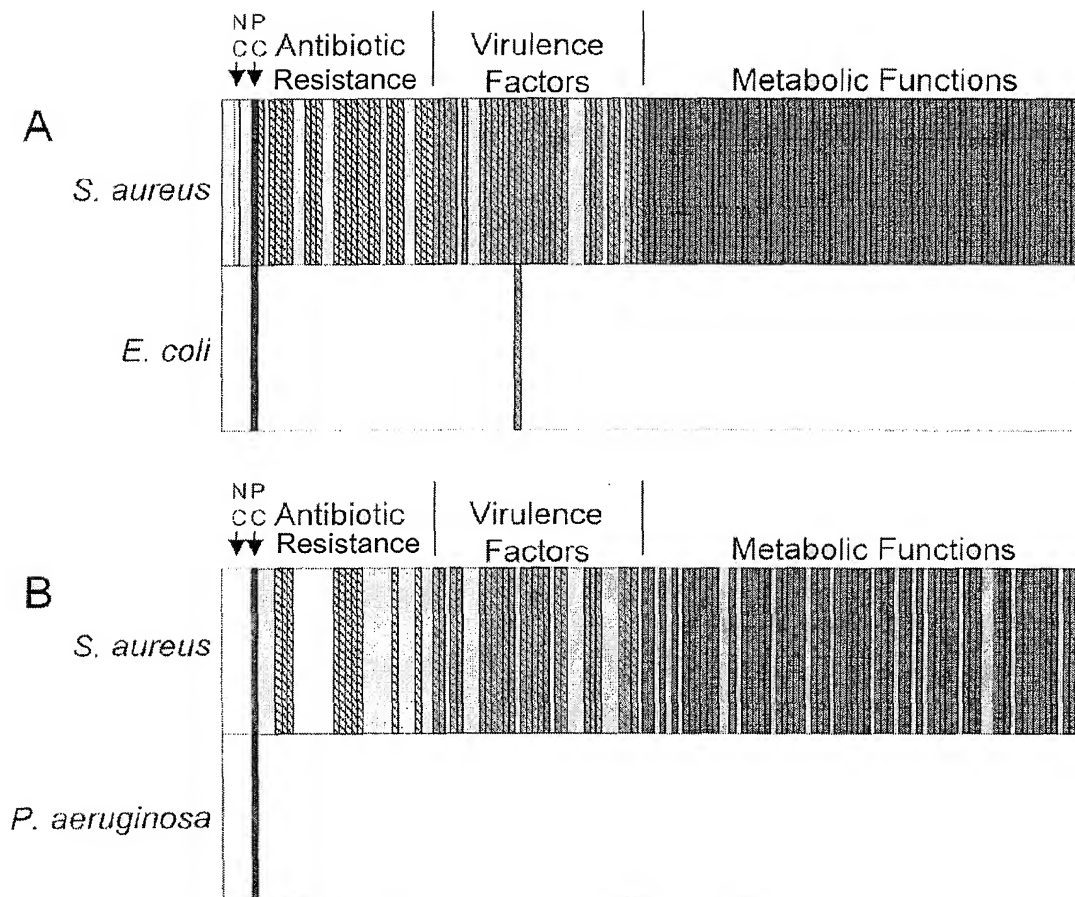


Fig.3

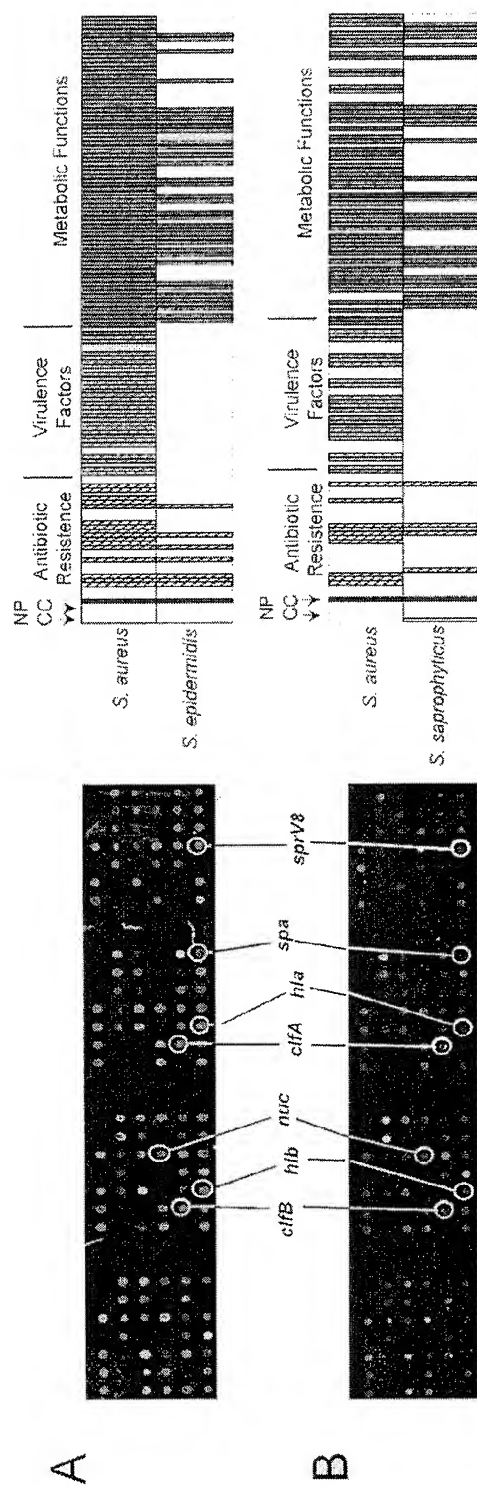


Fig.4

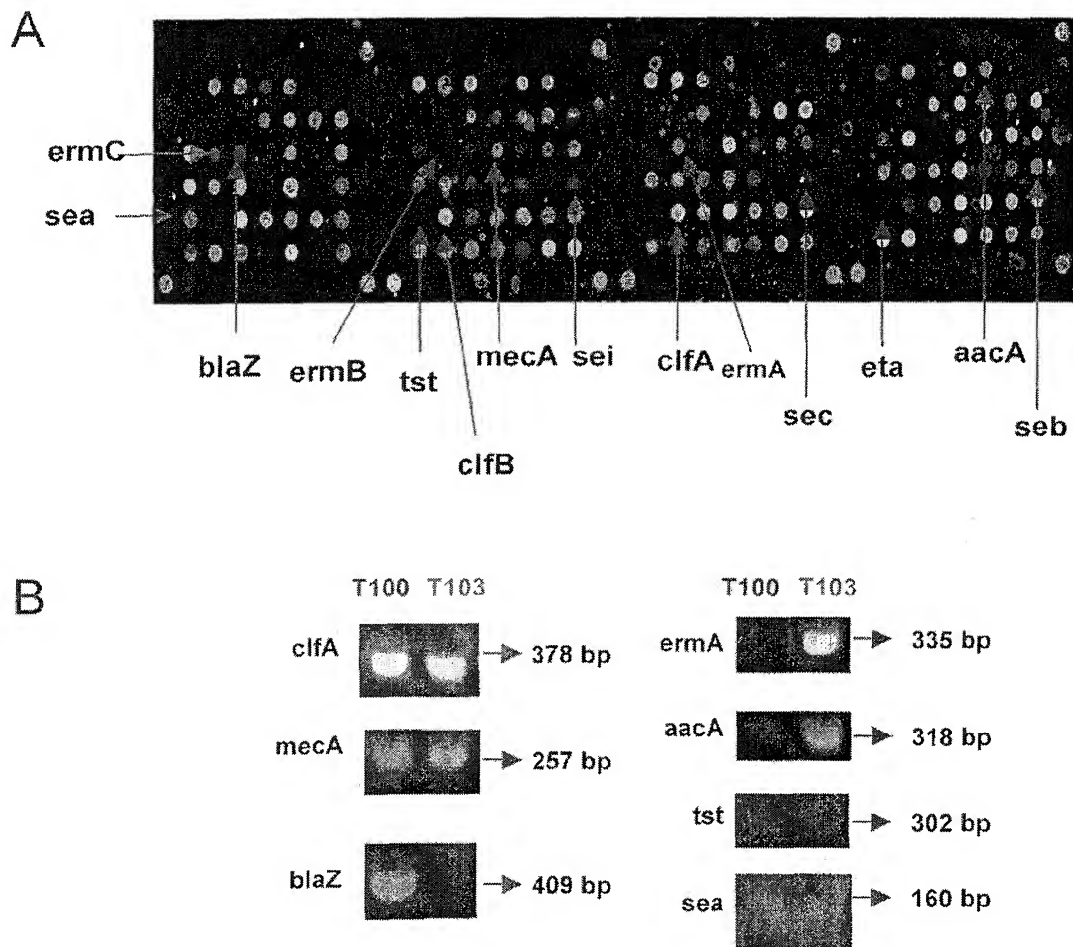


Fig.5

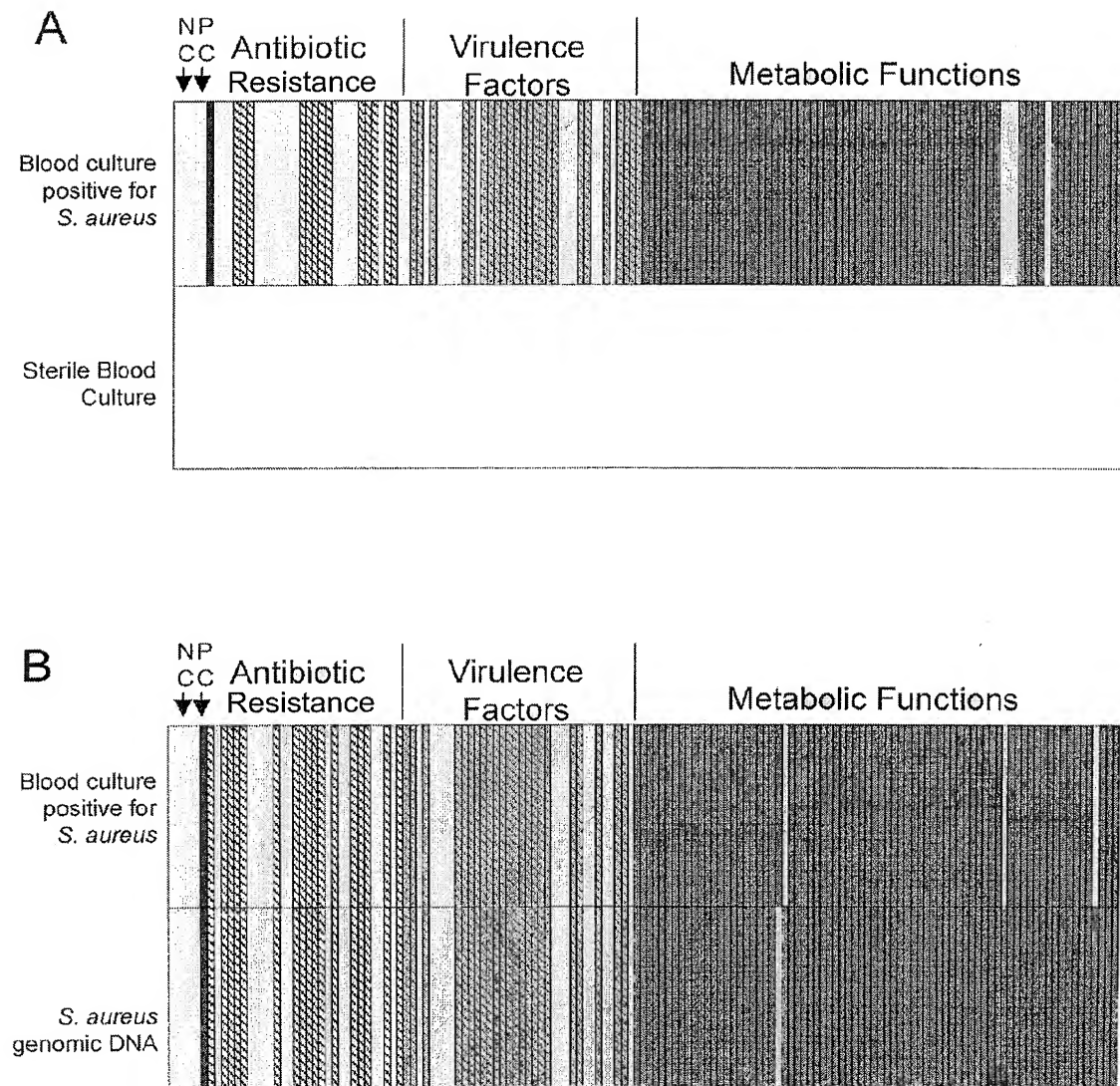


Fig.6



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PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 05 10 9025 shall be considered, for the purposes of subsequent proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
X	US 6 747 137 B1 (WEINSTOCK KEITH G ET AL) 8 June 2004 (2004-06-08) * paragraph [0244] * * paragraphs [0132], [0133] * * paragraph [0012] * * sequence 3589 *	1-11	INV. C12Q1/68
A	NAKAMURA M ET AL: "DEVELOPMENT OF THE DNA MICRO ARRAY FOR IDENTIFICATION OF INFECTIOUS DISEASE CAUSACTIVE BACTERIA IN HUMAN" 18 May 2003 (2003-05-18), ABSTRACTS OF THE GENERAL MEETING OF THE AMERICAN SOCIETY FOR MICROBIOLOGY, THE SOCIETY, WASHINGTON, DC, US, PAGE(S) ABSTRNOC219 , XP008047725 ISSN: 1060-2011 * abstract *	1-11	
A	EP 1 310 569 A (PRESIDENT OF GIFU UNIVERSITY) 14 May 2003 (2003-05-14) * claim 14 *	1-11	TECHNICAL FIELDS SEARCHED (IPC) C12Q
<p>----- -/--</p>			
INCOMPLETE SEARCH			
<p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>see sheet C</p>			
Place of search Munich		Date of completion of the search 19 December 2005	Examiner Helliot, B
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

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EPO FORM 1503 03.82 (P04C07)

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (IPC)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	WO 92/07096 A (MICROPROBE CORPORATION) 30 April 1992 (1992-04-30) * page 12, paragraph 2 * * page 27, paragraph 2 * * example 6 * -----	1-11	<div>TECHNICAL FIELDS SEARCHED (IPC)</div>
A	LEHNER A ET AL: "Oligonucleotide microarray for identification of Enterococcus species" 1 May 2005 (2005-05-01), FEMS MICROBIOLOGY LETTERS, AMSTERDAM, NL, PAGE(S) 133-142 , XP004876200 ISSN: 0378-1097 * abstract *	1-11	
A	WANG R-F ET AL: "DNA microarray analysis of predominant human intestinal bacteria in fecal samples" August 2004 (2004-08), MOLECULAR AND CELLULAR PROBES, ACADEMIC PRESS, LONDON, GB, PAGE(S) 223-234 , XP004522575 ISSN: 0890-8508 * abstract; tables 1,2 * -----	1-11	



Claim(s) searched completely:
1-5,7-21

Claim(s) searched incompletely:
6

Reason for the limitation of the search:

The present remarks apply to the only searched invention. If further search fees were paid, similar remarks could apply to the further searched inventions, leading to an incomplete search.

The present claim 6 relates to an DNA microarray suitable for the detection of *Staphylococcus aureus* and/or other microorganisms, among them *C. albicans*, using one or more or all gene probes listed as SEQ ID N° 1-909.

However, in view of the extremely large number of possible probes mentioned in the said claim, the said claim 6 lacks clarity and conciseness in the sense of Article 84 and a meaningful search of the whole claimed subject-matter of the claim could not be carried out (Rule 45 EPC and Guidelines B-VIII, 3).

The search of claim 6 was, thus, limited to the only microarray clearly disclosed in the application and suitable for the identification of *C. albicans*, namely the microarray comprising either the gene probe listed as SEQ ID N° 231 (irrespective of any other probes) or the whole of the genes listed as SEQ ID N° 1-909, and having a length of at least 100 nucleotides.



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CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

- ☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):
- ☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

- ☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.
- ☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.
- ☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:
- ☒ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

1-11 (all partially)



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: 1-11 (all partially)

A DNA microarray for direct identification of *Candida albicans* in a sample or clinical specimen, wherein the microarray comprises the gene probe listed as SEQ ID N° 231 or the whole of the genes listed as SEQ ID N° 1-909, and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 2-85: claims 1-11 (all partially)

A DNA microarray for direct identification of *Candida albicans* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 232 and 307 and between 910 and 918), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 86-278: claims 1-11 (all partially)

A DNA microarray for direct identification of *Enterococcus faecalis* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 308 and 376 and between 785 and 909), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 279-300: claims 1-11 (all partially)



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A DNA microarray for direct identification of *Enterococcus faecium* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 377 and 398), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 301-333: claims 1-11 (all partially)

A DNA microarray for direct identification of *Escherichia coli* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 142 and 173) or gene probes as listed in Tab. 2 of Example 4, and having a length of at least 10 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 334: claims 1-11 (all partially)

A DNA microarray for direct identification of *Klebsiella oxytoca* in a sample or clinical specimen, wherein the microarray comprises gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 449 and 469), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 335-384: claims 1-11 (all partially)



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A DNA microarray for direct identification of *Klebsiella pneumoniae* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 399 and 448), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 385: claims 1-11 (all partially)

A DNA microarray for direct identification of *Proteus mirabilis* and *vulgaris* in a sample or clinical specimen, wherein the microarray comprises gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 706 and 775 and between 776 and 784), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 386: claims 1-2, 8-11 (all partially)

A DNA microarray for direct identification of *Enterobacter cloacae* in a sample or clinical specimen.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 387-439: claims 1-11 (all partially)



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A DNA microarray for direct identification of *Pseudomonas aeruginosa* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 470 and 522), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 440: claims 1-2, 8-11 (all partially)

A DNA microarray for direct identification of *Stenotrophomonas maltophilia* in a sample or clinical specimen.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 441: claims 1-2, 8-11 (all partially)

A DNA microarray for direct identification of *Acinetobacter baumannii* in a sample or clinical specimen.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 442-581: claims 1-11 (all partially)

A DNA microarray for direct identification of *Staphylococcus aureus* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 1 and 141), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Inventions 582-616: claims 1-11 (all partially)

A DNA microarray for direct identification of *Staphylococcus epidermidis* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 174 and 208), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 617: claims 1-11 (all partially)

A DNA microarray for direct identification of *Staphylococcus haemolyticus* in a sample or clinical specimen, wherein the microarray comprises gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 209 and 215), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 618: claims 1-11 (all partially)

A DNA microarray for direct identification of *Staphylococcus lugdunensis* in a sample or clinical specimen, wherein the microarray comprises gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 216 and 221), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 619: claims 1-11 (all partially)



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A DNA microarray for direct identification of *Staphylococcus warneri* in a sample or clinical specimen, wherein the microarray comprises gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 224 and 230), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 620: claims 1-11 (all partially)

A DNA microarray for direct identification of *Streptococcus agalactiae* in a sample or clinical specimen, wherein the microarray comprises gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 606 and 644), and having a length of at least 100 nucleotides.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 621: claims 1-2, 8-11 (all partially)

A DNA microarray for direct identification of *Streptococcus bovis* in a sample or clinical specimen.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 622: claims 1-2, 8-11 (all partially)

A DNA microarray for direct identification of *Streptococcus dysgalactiae* in a sample or clinical specimen.

Use of the DNA microarray.

An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.

A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 623: claims 1-2, 8-11 (all partially)



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

A DNA microarray for direct identification of *Streptococcus mitis* in a sample or clinical specimen.
 Use of the DNA microarray.
 An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.
 A kit for the detection of microorganisms in a sample or clinical specimen.

Invention 624: claims 1-2, 8-11 (all partially)

A DNA microarray for direct identification of *Streptococcus mutans* in a sample or clinical specimen.
 Use of the DNA microarray.
 An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.
 A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 625-831: claims 1-11 (all partially)

A DNA microarray for direct identification of *Streptococcus pneumoniae* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 399 and 605), and having a length of at least 100 nucleotides.
 Use of the DNA microarray.
 An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.
 A kit for the detection of microorganisms in a sample or clinical specimen.

Inventions 832-873: claims 1-11 (all partially)

A DNA microarray for direct identification of *Streptococcus pyogenes* in a sample or clinical specimen, wherein the microarray comprises one gene probe selected among the gene probes listed as SEQ ID N° n (wherein n is an integer comprised between 645 and 686), and having a length of at least 100 nucleotides.
 Use of the DNA microarray.
 An in vitro method for identification and characterisation of microorganisms in a sample or in a clinical specimen.
 A kit for the detection of microorganisms in a sample or clinical specimen.

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 05 10 9025

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
The members are as contained in the European Patent Office EDP file on
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19-12-2005

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